FIGURE 1

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGA**ATG**GACTGGCCTCACAACCTGCTGTTTCTT
CTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG
GCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTCACGGATGAAACCGTATGCCC
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG
AGAAAGTGTGAGGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT
CAACCACGACCCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACC
CCTTCACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCCTGTGCGCCGCCGC
CTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG
CACCTGCATCTTC**TGA**ATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGACCATCCTCCTTGCACCTTT
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSMVSVP
VFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

FIGURE 3

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCCCCGGCCTCC
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC
GGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGG
TGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC
CAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC
GGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT
GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGT
G**TGA**CCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTG
TATTTATTGTTATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC
AGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCT
TACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTA
AACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLE
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRE
TAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV

Signal peptide:	Amino acids 1-18
Tyrosine kinase phosphorylation site:	Amino acids 112-121
N-myristoylation sites:	Amino acids 32-38;55-61;133-139
Leucine zipper pattern:	Amino acids 3-25
Homologous region to IL-17:	Amino acids 99-195

FIGURE 5

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCAGTCA
GTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCAGTGCAGAGGGCTGCCTGAGGGCT
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG
GGGCCAAGTGGAGTGAGAAACTGGGATCCCAGGGGGAGGGTGCAG**ATG**AGGGAGCGACCCAGATTAGGTGA
GGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCT
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA
CCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGA
CCTGTACCACGCCCGTTGCCTGTGCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGG
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACC
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGTGT
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG
CCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCTGTGAAGTGCTGTCTGGAGCAGCAGGATCCCGGGAC
AGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC
CGGAAGCTGGTGTCCTGTCATTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCCATTTCTGGAGGCCACCA
CTCCTGTCTCTTCCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACTTTCTAGATATTTCCCC
CTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATTTGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGG
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA
GAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPARPNRHP
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR
RPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide:	Amino acids 1-32
N-glycosylation site:	Amino acids 136-140
Tyrosine kinase phosphorylation site:	Amino acids 127-135
N-myristoylation sites:	Amino acids 44-50;150-156

FIGURE 7

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCCAGGGCGGGCAGGCG
CCCCGCGCGGCCGCGGGGCTGCGCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG
CCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC
CCGGCAGGGGGCAGGCCCGGCGACCGCCGCTTCCGGCCGCCCACCAACCTGCGCAGCGTGTCGCCCTGGGC
CTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCT
GCCTGACCGGGCTGTTCGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTC
CTGCGCCGCACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGG
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCTGAGGCCGGTCCTGCCCCGGGAGGTCTCCCCGG
CCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCCTGGAGGGCTCGGTCGGCGACCTCTGAAGAGAGTGCACC
GAGCAAACCAAGTGCCGGAGCACCAGCGCCGCCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGG
GCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC
GGCTGCTGCGGGTGCAGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT
AAAGCAATCTAAAAATAATAATAAGTATAGCGACTATATACCTACTTTTAAAATCAACTGTTTTGAATAGA
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTCTGG
CCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC
TTCCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCA
GGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACTCGC
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGA
ACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTTGCTGAAGGAT

FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC
PAGGRPGDRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVV
LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGAKLLLGPNDAPAGP

Signal peptide:	Amino acids 1-15
N-glycosylation sites:	Amino acids 68-72;181-185
Tyrosine kinase phosphorylation site:	Amino acids 97-106
N-myristoylation sites:	Amino acids 17-23;49-55;74-80; 118-124
Amidation site:	Amino acids 21-25

FIGURE 9

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAAC**ATG**ACAGTGAAGACCCTGCATGGCCCAGCCAT
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACTTGG
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCTGGTGACTGTTGGCTGCACCTG
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

FIGURE 10

MTVKTLHGPAMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS
RNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:	Amino acids 1-30
N-glycosylation site:	Amino acids 83-86
N-myristoylation sites:	Amino acids 106-111;136-141

FIGURE 11

CCGGCG**ATG**TCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGACTTGA
GGGACCTCCGAGTAGAACCTGTTACAACTAGTGTTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAA
CTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTG
GTAAATGGACATTTTCCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCATTGGGGCCCATAAT
ATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGA
CCACATAATGAAATATAAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTA
AGAAGAATGAGGAGACAGTAGAAGTGAACTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATC
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCA
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAAC
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC
CCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA
TTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGG
TCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCA
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC
CTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTT
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGC
CACGATGGCTGCTGCTCCTTGTAG

FIGURE 12

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHD
GCCSL

Signal sequence: Amino acids 1-14

Transmembrane domain: Amino acids 290-309

N-glycosylation sites: Amino acids 67-70;103-106;156-159;
183-186;197-200;283-286

cAMP- and cGMP-dependent protein kinase phosphorylation sites:
Amino acids 228-231;319-322

N-myristoylation site: Amino acids 116-121

Amidation site: Amino acids 488-491

FIGURE 13

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG
AGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCTGCCA
CCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCCTTGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGT
GCCACCTGGCACCTAGAAG**ATG**CCTGTGCCCTGGTTCTTGCTGTCCTTGGCACTGGGCCGAAGCCCAGTGG
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTC
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCA
CCTGCAGACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCG
CTGCGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGGA
ACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCAGCAGATGGTGACAACGTGCATC
TGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCA
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG
CCTCTGTATTCAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCTTCAGGGAGGACC
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC
GCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT
GGTCCCACCGCTTTCCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCACC
CTAACCTCTGTGTTCAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTG
GGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTT
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTC
CCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGG
GGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG
GGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCGTGAACT
GAGCGCGCAGGGGCCCGTGGCTTGGTTTCACGCGCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGG
TCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGG
GCGCACGGCCCGCACGACGCCTTCCGCGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGCAGGGCCGGGC
GCCCGGCAGCTACGTGGGGGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCA
CCGTGCCCGTCTTCACACTGCCCTCCCAACTGCCAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCG
CGTTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTT
CCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGGACGGGA
CTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAAA

FIGURE 14

MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVS
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKGWLRLLKQDVRSGAAARG
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

signal sequence:	Amino acids 1-20
transmembrane domain:	Amino acids 453-473
N-glycosylation sites:	Amino acids 118-121;186-189;198-201; 211-214;238-241;248-251;334-337; 357-360;391-394
Glycosaminoglycan attachment site:	Amino acids 583-586
cAMP- and cGMP-dependent protein kinase phosphorylation site:	Amino acids 552-555
N-myristoylation sites:	Amino acids 107-112;152-157;319-324; 438-443;516-521;612-617;692-697; 696-701;700-705

FIGURE 15

CGAGGGCTCCTGCTGGTACTGTGTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCC**ATG**GGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTCGCCACCTGCCCCACTGGAACACC
CGCTGTCCTCTGGCCTCCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGC
TGTCAGGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAAGTCTTCCACA
TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTCACCTGTC
TGAGAAGAGCCATCACATTTCCATCCCCTCCCCAGACATCTCCCACAAGGGACTTCGCTCTAAAAGGACCC
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACAAAGGCATGGAGGACCCGAGTTC
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCGGGTGACCATATCTTCAGGCCCTGAGGTCAGCGTGCG
TCTTTGTCACCAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG
GGGGCCACACTGTAGAGCTGCCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAA
GAGGACACTGTGAGGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA
GTCAGTGCACTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCACTGA
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATACCCTTTGCAAAGACCTCCCGAATGCCACGGCT
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTTCAAGTTCTCTTT
TGGAAACAGCAGCCATGTTGAATGCCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTC
CCAGGCTTGGGGCAGGACACTTTGGTGCCCCCCGTGTACACTGTCAGCCAGGCCCGGGGCTCAAGCCCAGT
GTCACTAGACCTCATCATTCCCTTCCTGAGGCCAGGGTGCTGTGTCCTGGTGTGGCGGTCAGATGTCCAGT
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG
GCCCTCCTCACCCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCCACAGTCAGGCCCGGGCCCAGC
GCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGGCGCCTGGTGGGAGCGCTGGCTGAAC
TGCTACGGGCAGCGCTGGGCGGCGGGCGCGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT
GGGCCCGCTGCCGTGGCTCTGGGCGGCGCGGACGCGCGTAGCGCGGGAGCAGGGCACTGTGCTGCTGCTGT
GGAGCGGCGCCGACCTTCGCCCGGTCAGCGGCCCCGACCCCCGCGCCGCGCCCCTGCTCGCCCTGCTCCAC
GCTGCCCCGCGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCCGCC
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGGACGCGCGGC
CTTTCGCAGAGGCCACCAGCTGGGGCCGCCTTGGGGCGCGGCAGCGCAGGCAGAGCCGCCTAGAGCTGTGC
AGCCGGCTTGAACGAGAGGCCGCCCGACTTGCAGACCTAGGTTGAGCAGAGCTCCACCGCAGTCCCGGGTGTCT

FIGURE 16

MGSSRLAALLLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFTGSSAYIPCRTWWALFSTKPWCV
RVWHCSRCLCQHLLSGGSGLQRGLFHLLVQKSKKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS
PDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH
TQMVMALTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH
QTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR
PGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCRRPQSGPGPARPVLLLHAAD
SEAQRRLVGALAELLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLLWSGADLRPVS
GPDPRAAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPPLRALPRYRLLRDLPRLLRALDARPFAEATSWGR
LGARQRRQSRLELCSRLEREAARLADLG

Signal peptide: Amino acids 1-23

Transmembrane domain: Amino acids 455-472

N-glycosylation sites: Amino acids 318-322;347-351;364-368

Glycosaminoglycan attachment site: Amino acids 482-486

cAMP- and cGMP-dependent protein kinase phosphorylation sites: Amino acids 104-108;645-649

Tyrosine kinase phosphorylation site: Amino acids 322-329

N-myristoylation sites: Amino acids 90-96;358-364;470-476

Eukaryotic cobalamin-binding proteins: Amino acids 453-462

FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGGAGTGGGGGAGGTCAGACGGGGCGGTTGGAGGGGGAGGG**AT**
GCCACGCGCTTCTGCCTCAGGTGTTCCTGCGTTGTTTGTCAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA
GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAG
CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT
TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGT
CGGAGGGAAGACAGTGCCAACAACTGATTCTAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACT
GGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTTCC
TTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC
CGGACAATCTAGCTTGTAAACCCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC
AGGTGTCCTTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCCTTCGACCACGCACCGCACAACTTC
GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCA
GGAGCAAACTACAGAGATGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG
TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGG
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGAT
GTGCCGCAAGAAGCAACAAGAAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA
CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGC
CAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT
GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTCATCCAGAAGATCCACGAGT
CCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA
GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCG
CCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCCTGCGAGG
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCCTCAGCTCTGTTCC
CACCTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACTA
CTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGC
CCGACTGGTTCGAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAG
AAATTTGATTCGGGCTTGGTTTTAAATGATGTCATGTGCAAACCAGGGCCTGAGAGTGACTTCTGCCTAAA
GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGCCTGG
ACCAAGACGGGGAGGCCCGGCCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAA
GCCGGCAGCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCCTCCT
CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCCTTCCAAGCTCCTCTCTTCTGGGTCATGCAAAGCA
GATCTTGGTTGCCGCAGCTACACTGATGAACTCCACGCGGTCGCCCCTTTGTAACAAAACGAAAGAGTCTA
AGCATTGCCACTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MPRASASGVPALFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT
ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN
FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA
GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD
GQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKH
KGGGRGSGKGELFLVAVSAIAEKLRQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLSTKYRLMDNLPQLC
SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYVAICNMHQFIDEEPDWFEKQFVPFHPPPLRYREPVL
EKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAALQPLLHTV
KAGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPPALPSKLLSSGSCK
ADLGCRSYTDELHAVAPL

Transmembrane domain: Amino acids 283-307

N-glycosylation sites: Amino acids 31-34;38-41;56-59;
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:
Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site: Amino acids 19-24;375-380;428-433;
429-434;432-437;517-522;574-579;
652-657;707-712

```
h-IL17    1   ---------------------MTPGKTSLVSLLLLLSLEAIVKAGITIPR
h-IL17B   1   --------MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGP
h-IL17C   1   MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPH
h-IL17D   1   ---------------MLVAGFLLALPPSWAAGAPRAGRRPARPRGCADRP
h-IL17E   1   ---------------MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSH
h-IL17F   1   -------------MTVKTLHGPAMVKYLLLSILGLAFLSEAAARKIPKVG

h-IL17    30  NPGCPNSEDKNFPRTVMVNLNIHNRNTNTNPK--------------RSSD
h-IL17B   43  HQVPLDLVSRMKPYARMEEYERNIEEMVAQLRNSSELAQRKCEVNLQLWM
h-IL17C   51  LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEAD
h-IL17D   36  EELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASCPAGGRPADRRFRPP
h-IL17E   36  WPSCCPSKGQDTSEELLRWSTVPVPPLEPARPNRHPESCRAS----EDGP
h-IL17F   38  HTFFQKPESCPPVPGGSMKLDIGIINENQRVS--------------MSRN

h-IL17    66  YYNRSTSPWNLHRNEDPERYPSVIWEAKCRHLGCINAD-GNVDYHMNSVP
h-IL17B   93  SNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSMVSVP
h-IL17C   101 THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVR
h-IL17D   86  TNLRSVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFRSAP
h-IL17E   82  LNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSE
h-IL17F   74  IESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQ-GKEDISMNSVP

h-IL17    115 IQQEILVLRRE---------PPHCPNSFRLEKILVSVGCTCVTPIVHHVA
h-IL17B   143 VFSQVPVRRRLCPPP-----PRTGPCRQRAVMETIAVGCTCIF-------
h-IL17C   151 LLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV---
h-IL17D   136 VYMPTVVLRRTPACAG-------GRSVYTEAYVTIPVGCTCVPEPEKDAD
h-IL17E   132 LLYHNQTVFYRRPCHGEK--GTHKGYCLERRLYRVSLACVCVRPRVMG--
h-IL17F   123 IQQETLVVRRK---------HQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

h-IL17D   179 SINSSIDKQGAKLLLGPNDAPAGPX
```

FIG. 19

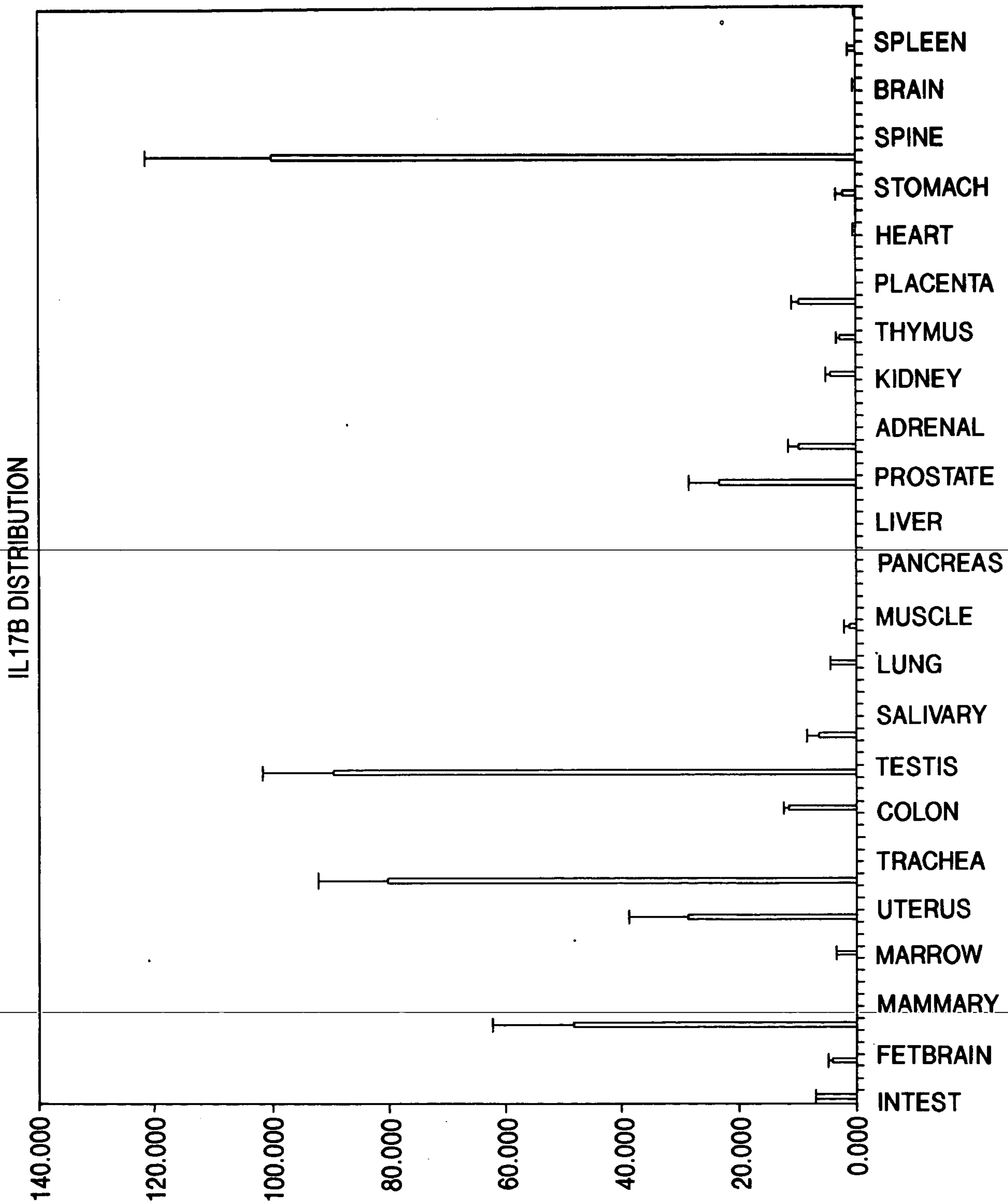

IL17B DISTRIBUTION
140.000
120.000
100.000
80.000
60.000
40.000
20.000
0.000
SPLEEN
BRAIN
SPINE
STOMACH
HEART
PLACENTA
THYMUS
KIDNEY
ADRENAL
PROSTATE
LIVER
PANCREAS
MUSCLE
LUNG
SALIVARY
TESTIS
COLON
TRACHEA
UTERUS
MARROW
MAMMARY
FETBRAIN
INTEST

FIG. 20

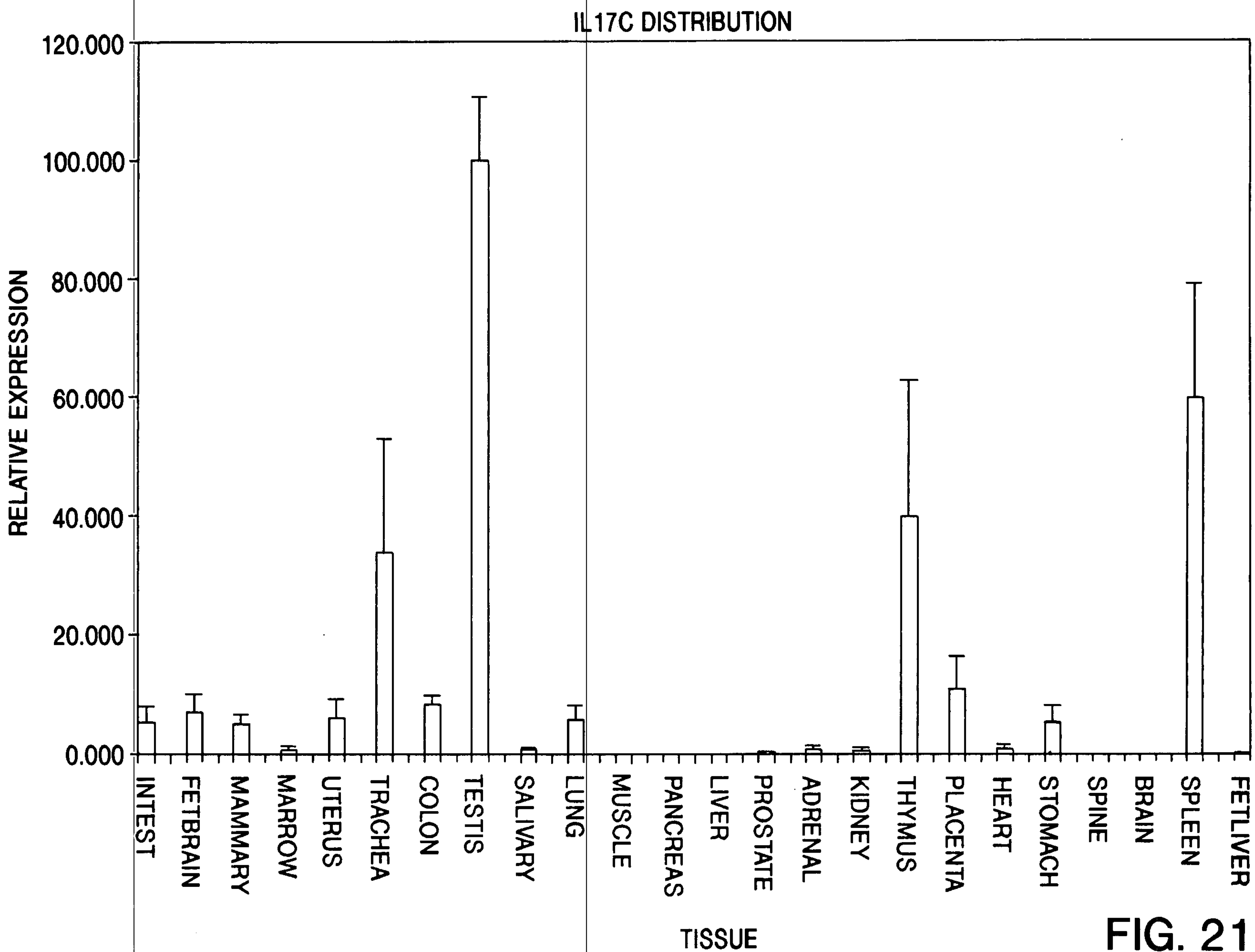

IL17C DISTRIBUTION
RELATIVE EXPRESSION
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
TRACHEA
COLON
TESTIS
SALIVARY
LUNG
MUSCLE
PANCREAS
LIVER
PROSTATE
ADRENAL
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE

FIG. 21

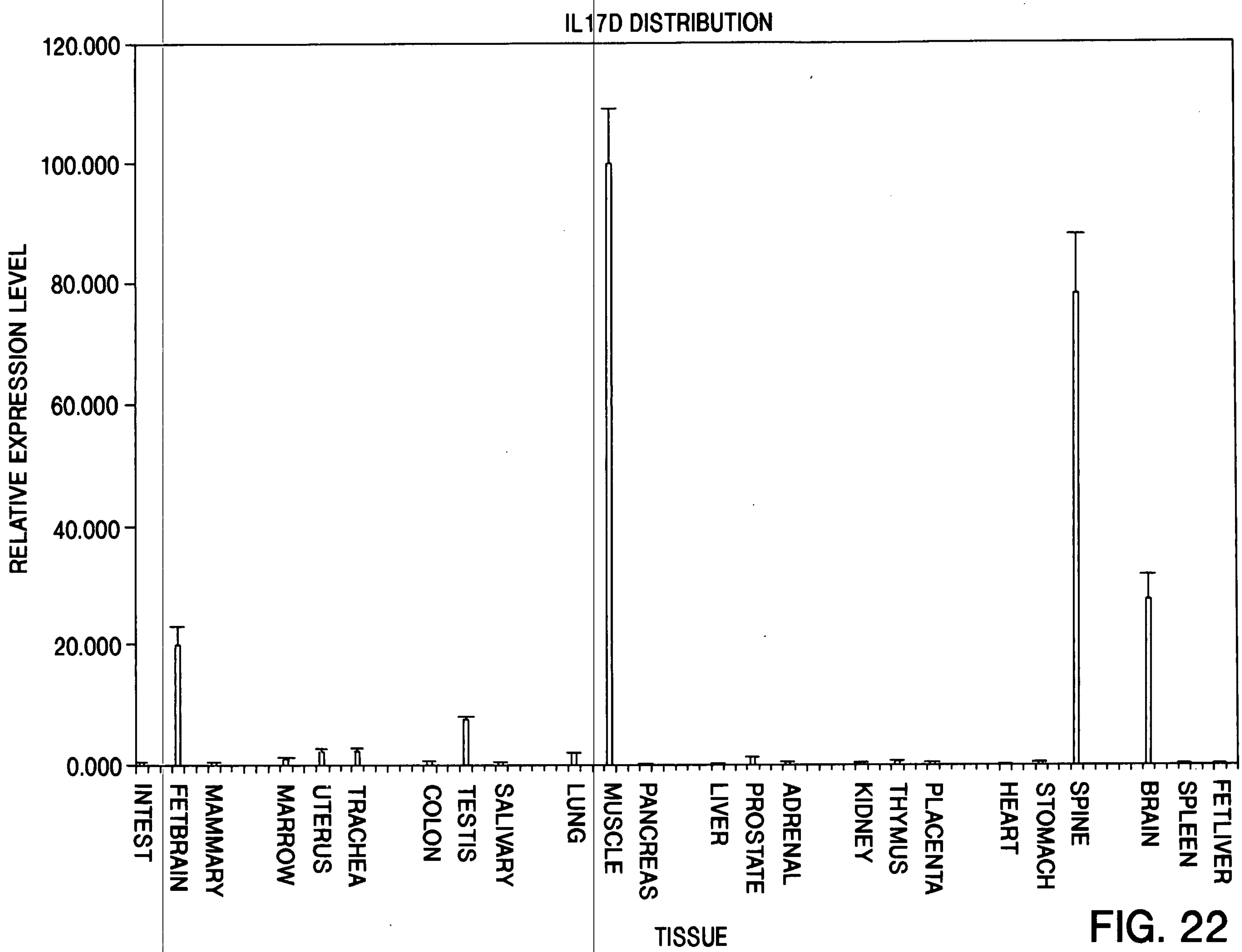

IL17D DISTRIBUTION
RELATIVE EXPRESSION LEVEL
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
TRACHEA
COLON
TESTIS
SALIVARY
LUNG
MUSCLE
PANCREAS
LIVER
PROSTATE
ADRENAL
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE

FIG. 22

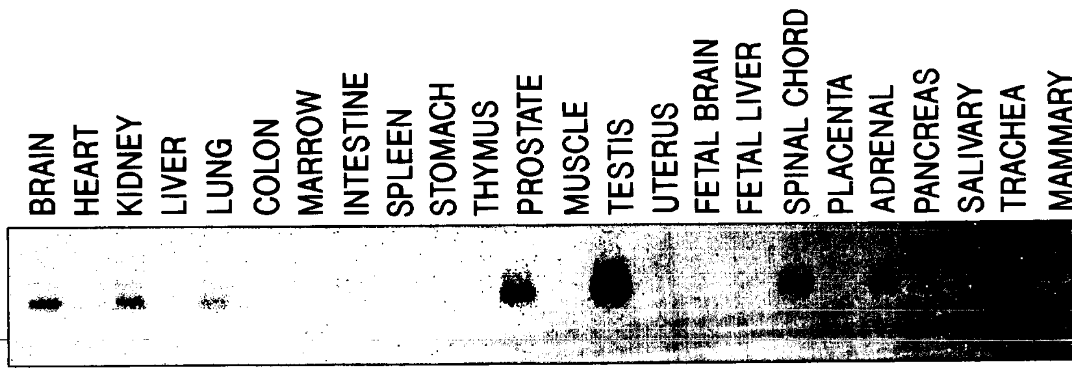

BRAIN
HEART
KIDNEY
LIVER
LUNG
COLON
MARROW
INTESTINE
SPLEEN
STOMACH
THYMUS
PROSTATE
MUSCLE
TESTIS
UTERUS
FETAL BRAIN
FETAL LIVER
SPINAL CHORD
PLACENTA
ADRENAL
PANCREAS
SALIVARY
TRACHEA
MAMMARY

FIG. 23

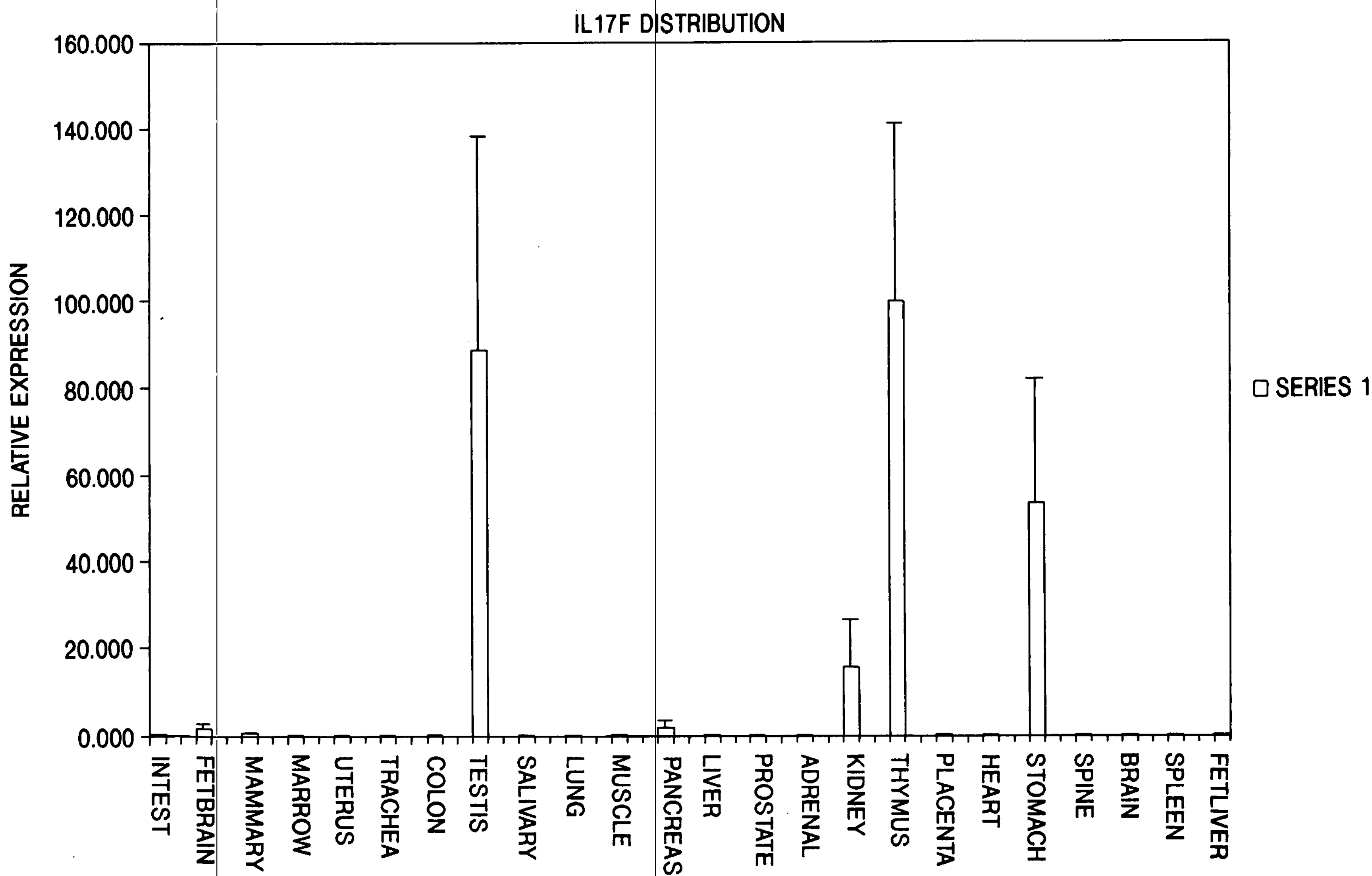

IL17F DISTRIBUTION
RELATIVE EXPRESSION
160.000
140.000
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
TRACHEA
COLON
TESTIS
SALIVARY
LUNG
MUSCLE
PANCREAS
LIVER
PROSTATE
ADRENAL
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE
SERIES 1

FIG. 24

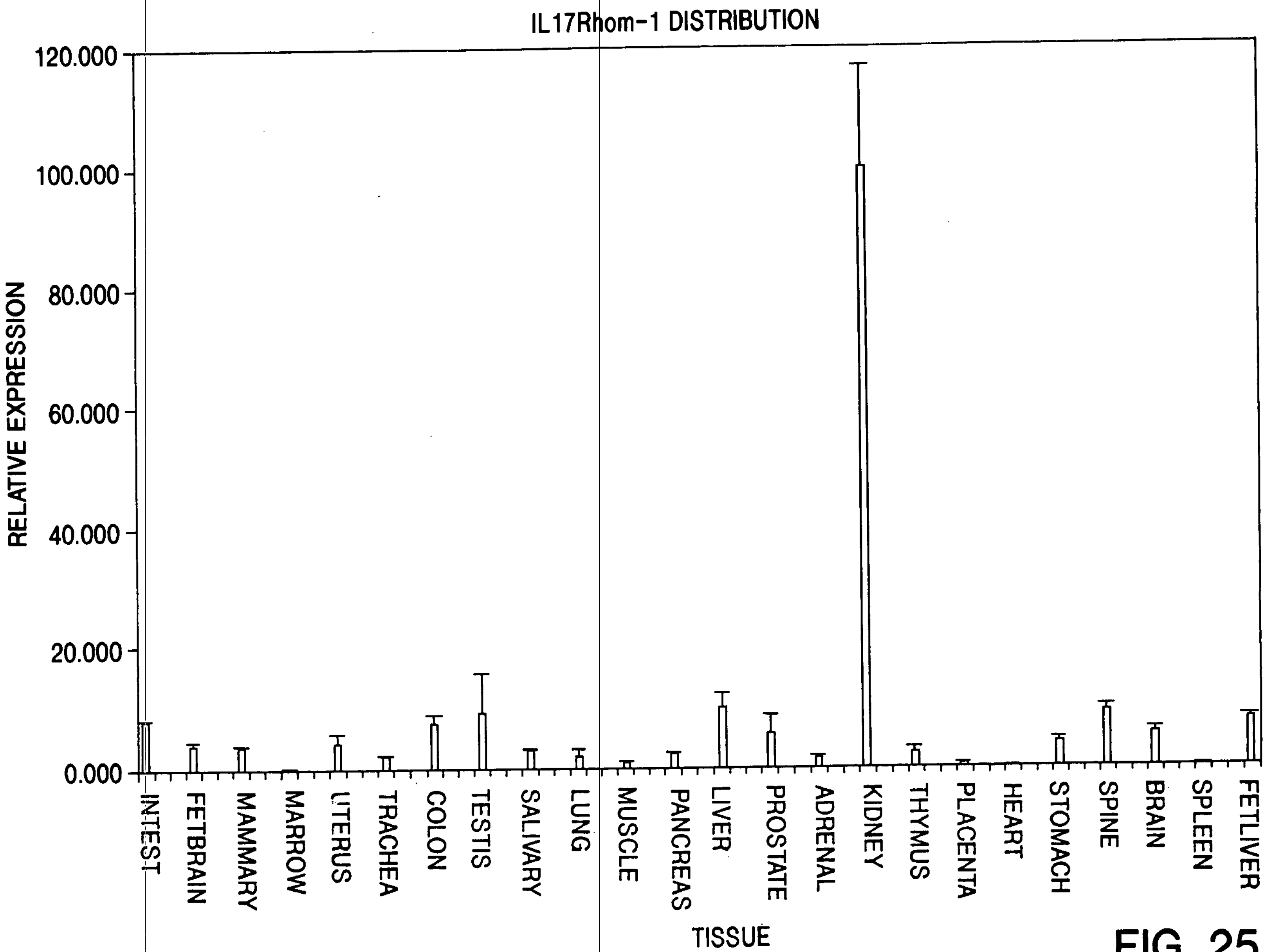

IL17Rhom-1 DISTRIBUTION
RELATIVE EXPRESSION
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
TRACHEA
COLON
TESTIS
SALIVARY
LUNG
MUSCLE
PANCREAS
LIVER
PROSTATE
ADRENAL
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE

FIG. 25

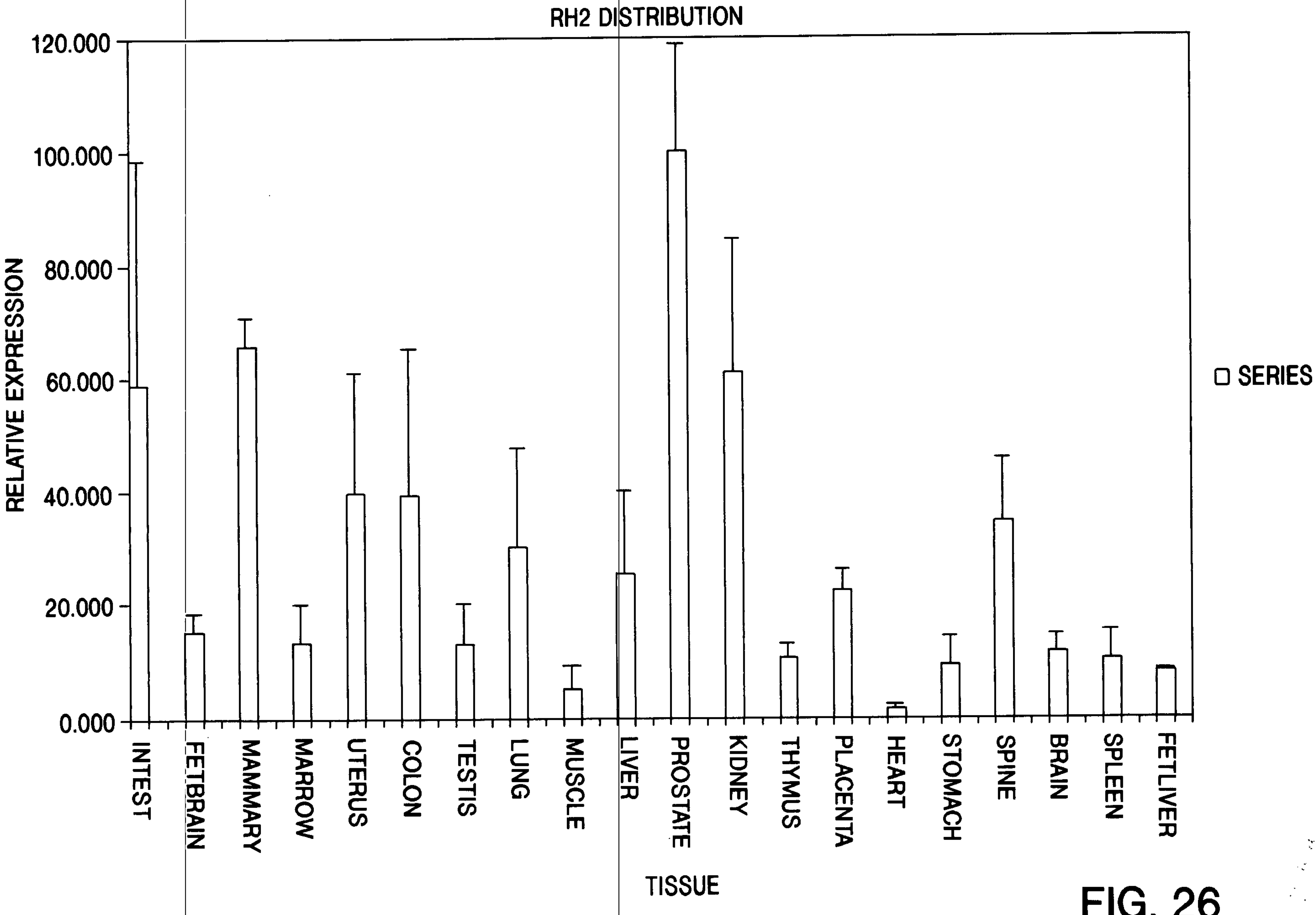

RH2 DISTRIBUTION
RELATIVE EXPRESSION
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
COLON
TESTIS
LUNG
MUSCLE
LIVER
PROSTATE
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE
SERIES

FIG. 26

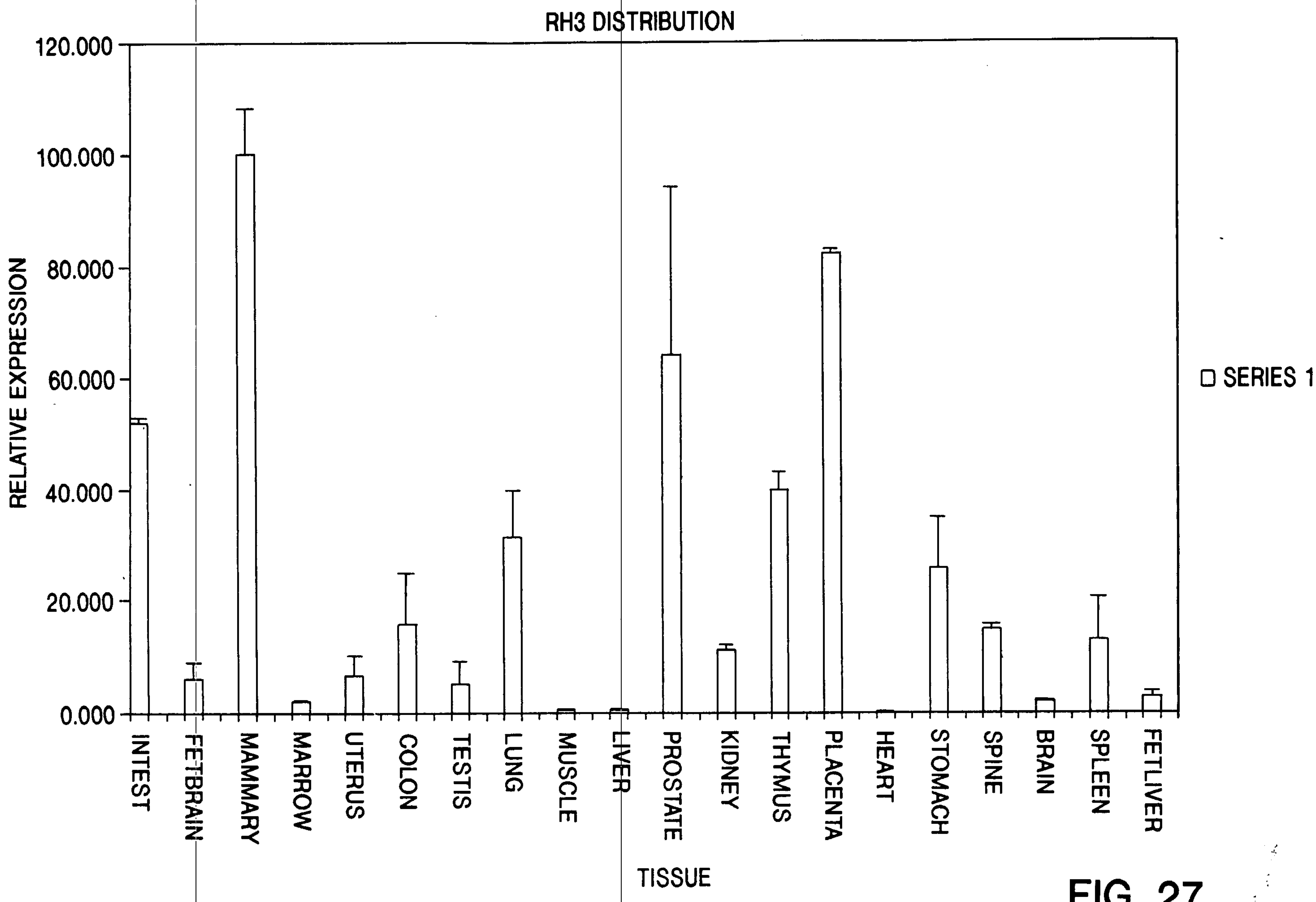

RH3 DISTRIBUTION
RELATIVE EXPRESSION
120.000
100.000
80.000
60.000
40.000
20.000
0.000
SERIES 1
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
COLON
TESTIS
LUNG
MUSCLE
LIVER
PROSTATE
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE

FIG. 27

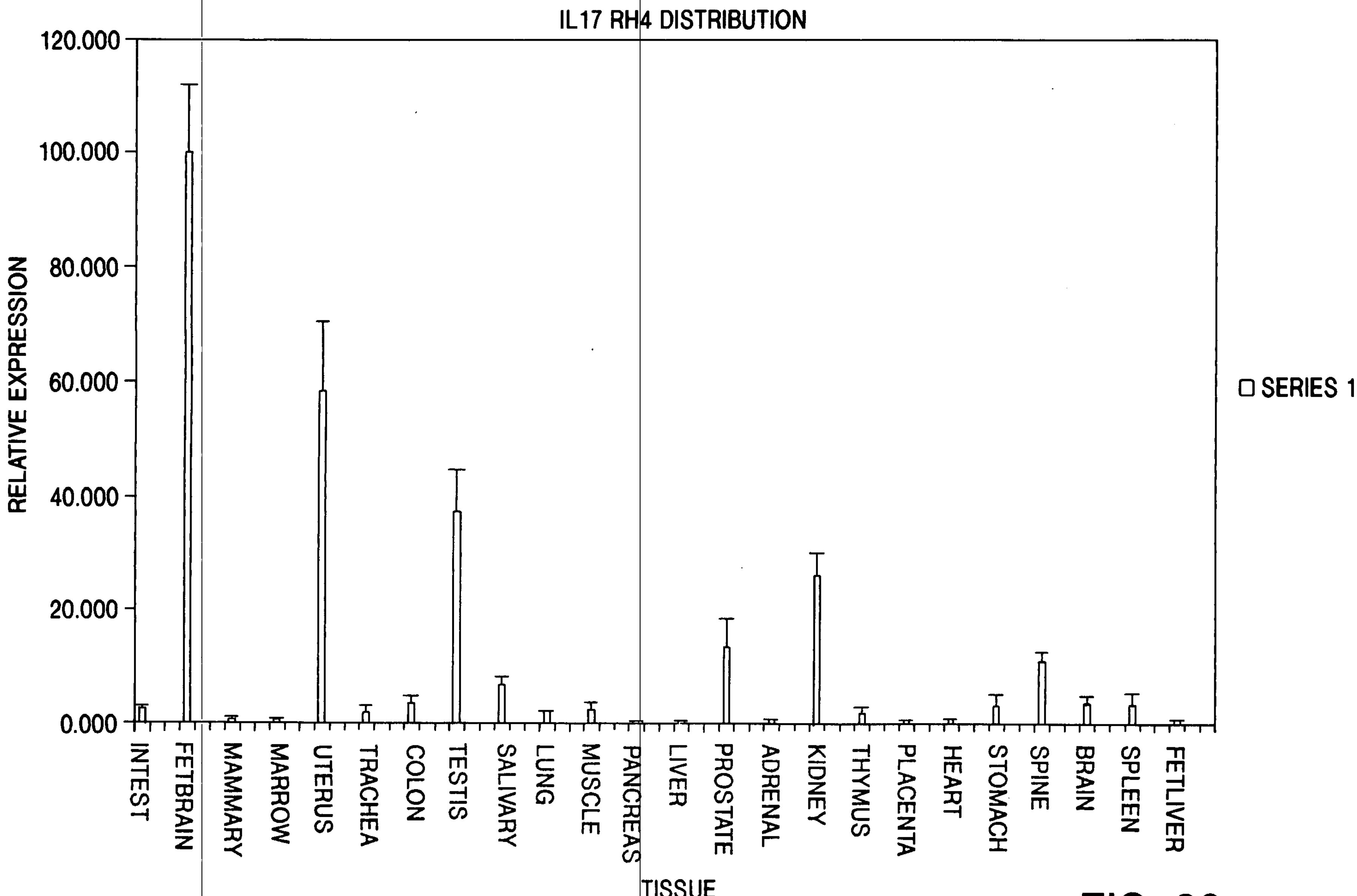

IL17 RH4 DISTRIBUTION
RELATIVE EXPRESSION
120.000
100.000
80.000
60.000
40.000
20.000
0.000
INTEST
FETBRAIN
MAMMARY
MARROW
UTERUS
TRACHEA
COLON
TESTIS
SALIVARY
LUNG
MUSCLE
PANCREAS
LIVER
PROSTATE
ADRENAL
KIDNEY
THYMUS
PLACENTA
HEART
STOMACH
SPINE
BRAIN
SPLEEN
FETLIVER
TISSUE
SERIES 1

FIG. 28

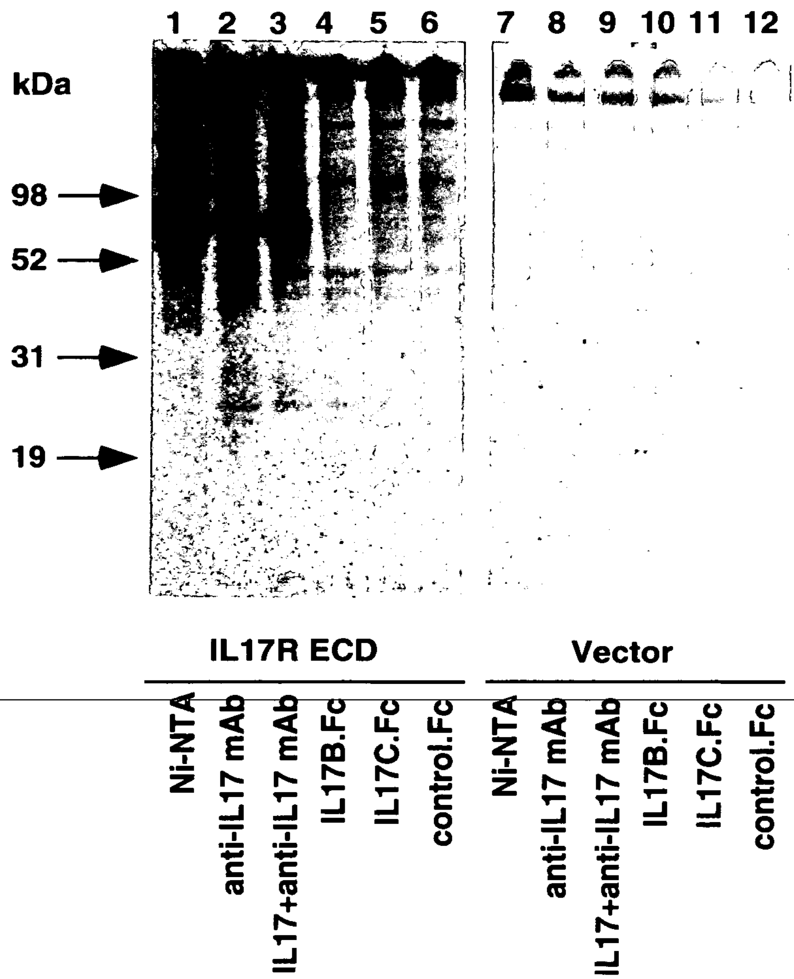


FIG. 29A

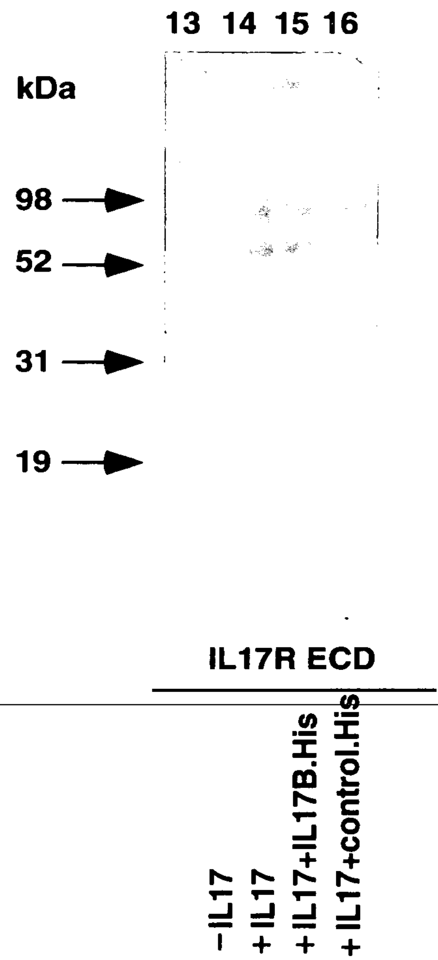


FIG. 29B

```
h-IL17     1   ------MTPGKTSLVSLLLLLSLEAIVKAGITIPR----------------
h-IL17B    1   ----MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGP---------L
h-IL17C    1   ----MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQ
h-IL17E    1   MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCP---------

h-IL17     30  -------------NPGCPNSEDKNFPRTVMVNLNIHNRNTNTNPKR-----
h-IL17B    39  APGPHQVPLDLVSRMKPYARMEEYERNIEEMVAQLRNSSELAQRKCEVNL
h-IL17C    47  APPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEV
h-IL17E    42  ------------SKGQDTSEELLRWSTVPVPPLEPARPNRHPESCRASE-

h-IL17     63  -SSDYYNRSTSPWNLHRNEDPERYPSVIWEAKCRHLGCINADG--NVDYH
h-IL17B    89  QLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSM
h-IL17C    97  LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTG-RETAA
h-IL17E    79  -DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPR

h-IL17     110 MNSVPIQQEILVLRRE----------PPHCPNSFRLEKILVSVGCTCVTPI
h-IL17B    139 VSVPVFSQVPVRRRLCPPP------PRTGPCRQRAVMETIAVGCTCIF--
h-IL17C    146 LNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPR
h-IL17E    128 GNSELLYHNQTVFYRRPCHGEK---GTHKGYCLERRLYRVSLACVCVRPR

h-IL17     151 VHHVA
h-IL17C    196 SV---
h-IL17E    175 VMG--
```

FIG. 30

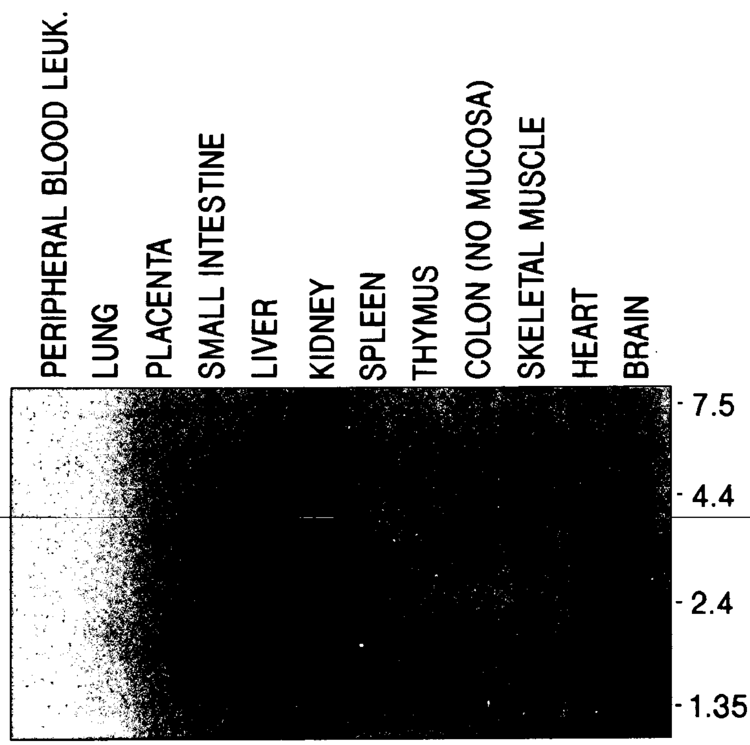
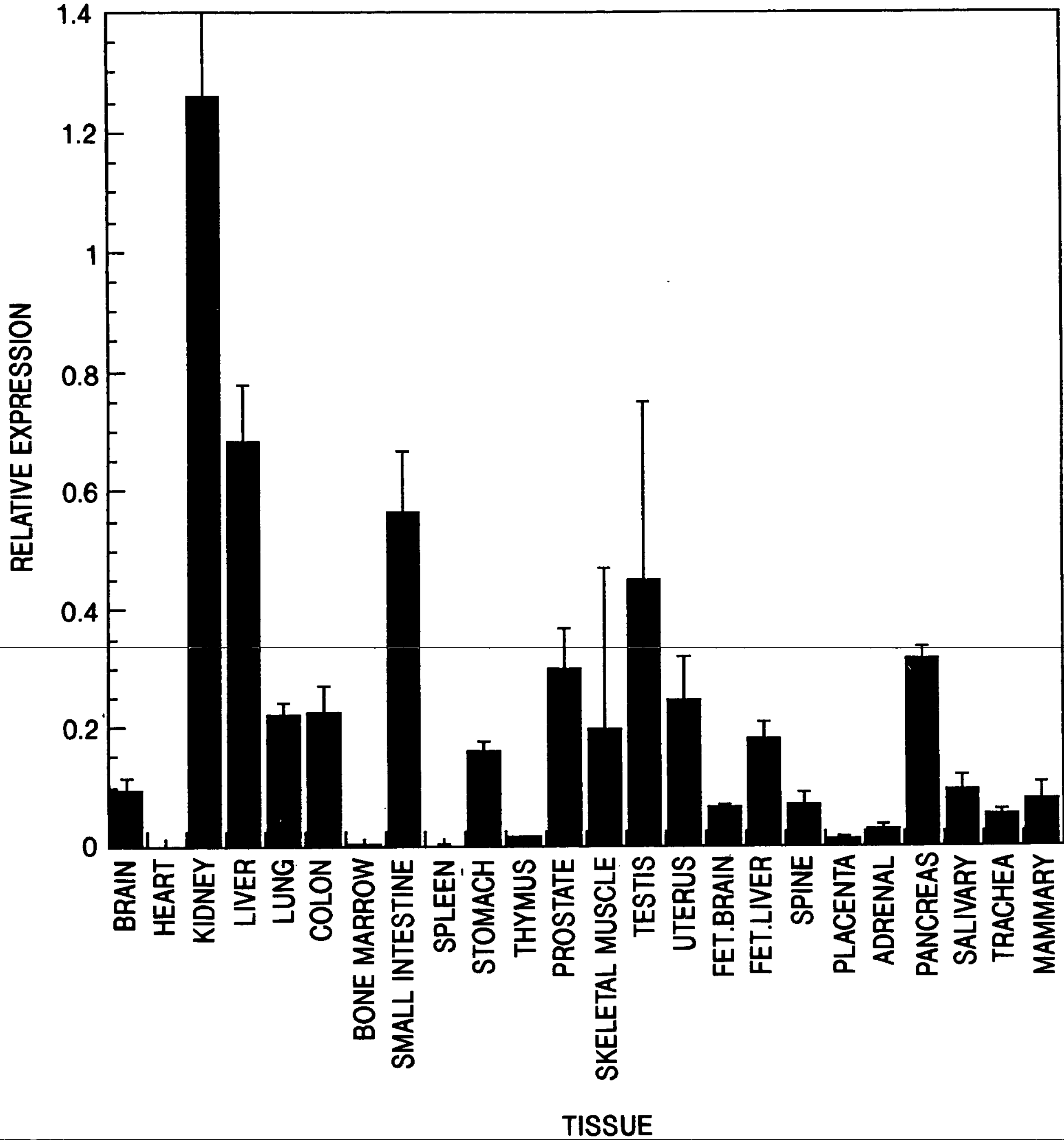

PERIPHERAL BLOOD LEUK.
LUNG
PLACENTA
SMALL INTESTINE
LIVER
KIDNEY
SPLEEN
THYMUS
COLON (NO MUCOSA)
SKELETAL MUSCLE
HEART
BRAIN
7.5
4.4
2.4
1.35

FIG. 31A



RELATIVE EXPRESSION
1.4
1.2
1
0.8
0.6
0.4
0.2
0
BRAIN
HEART
KIDNEY
LIVER
LUNG
COLON
BONE MARROW
SMALL INTESTINE
SPLEEN
STOMACH
THYMUS
PROSTATE
SKELETAL MUSCLE
TESTIS
UTERUS
FET.BRAIN
FET.LIVER
SPINE
PLACENTA
ADRENAL
PANCREAS
SALIVARY
TRACHEA
MAMMARY
TISSUE

FIG. 31B

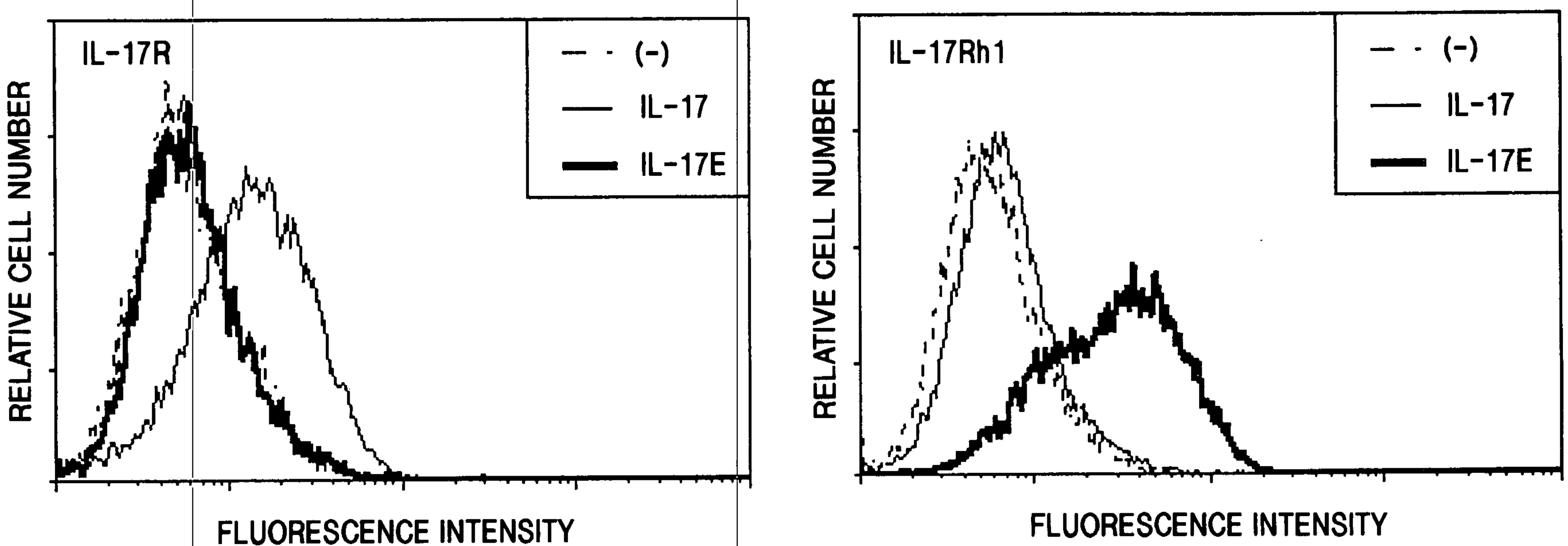

IL-17R
(-)
IL-17
IL-17E
RELATIVE CELL NUMBER
FLUORESCENCE INTENSITY
IL-17Rh1
(-)
IL-17
IL-17E
RELATIVE CELL NUMBER
FLUORESCENCE INTENSITY

FIG. 32A

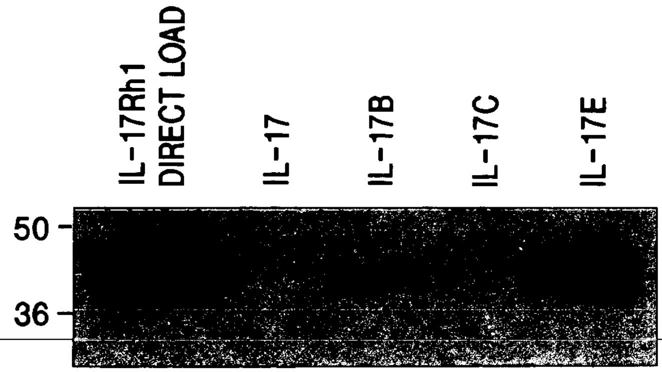


FIG. 32B

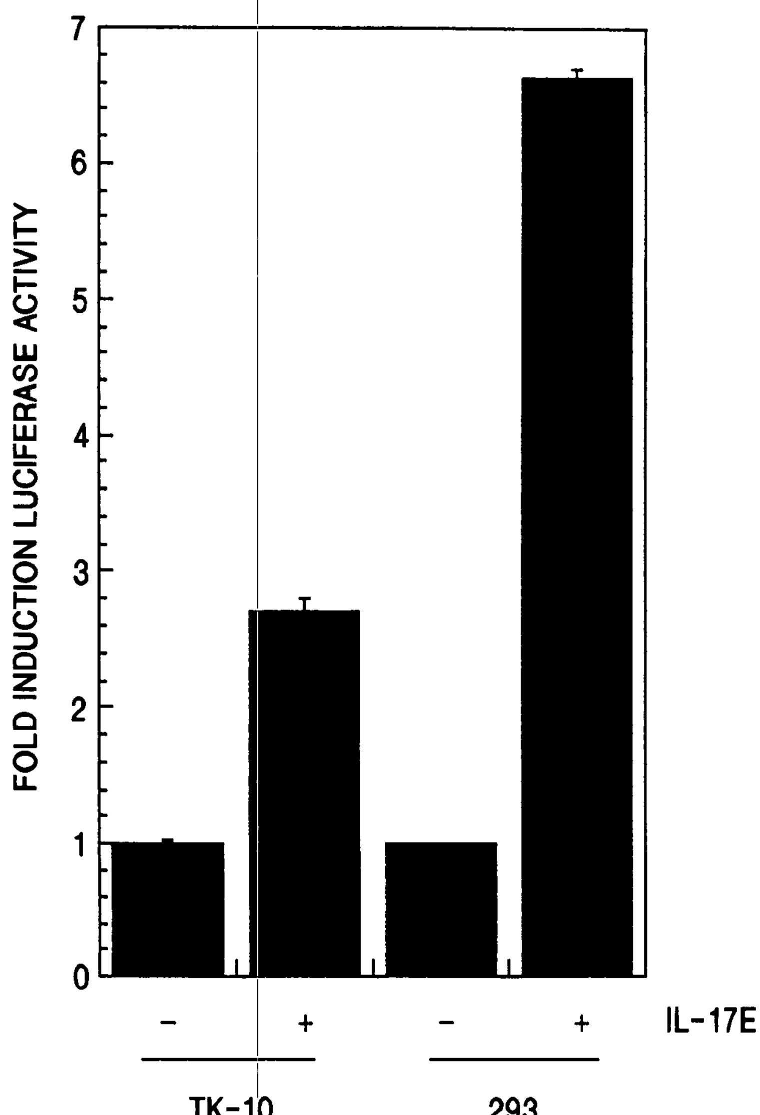


FIG. 33A

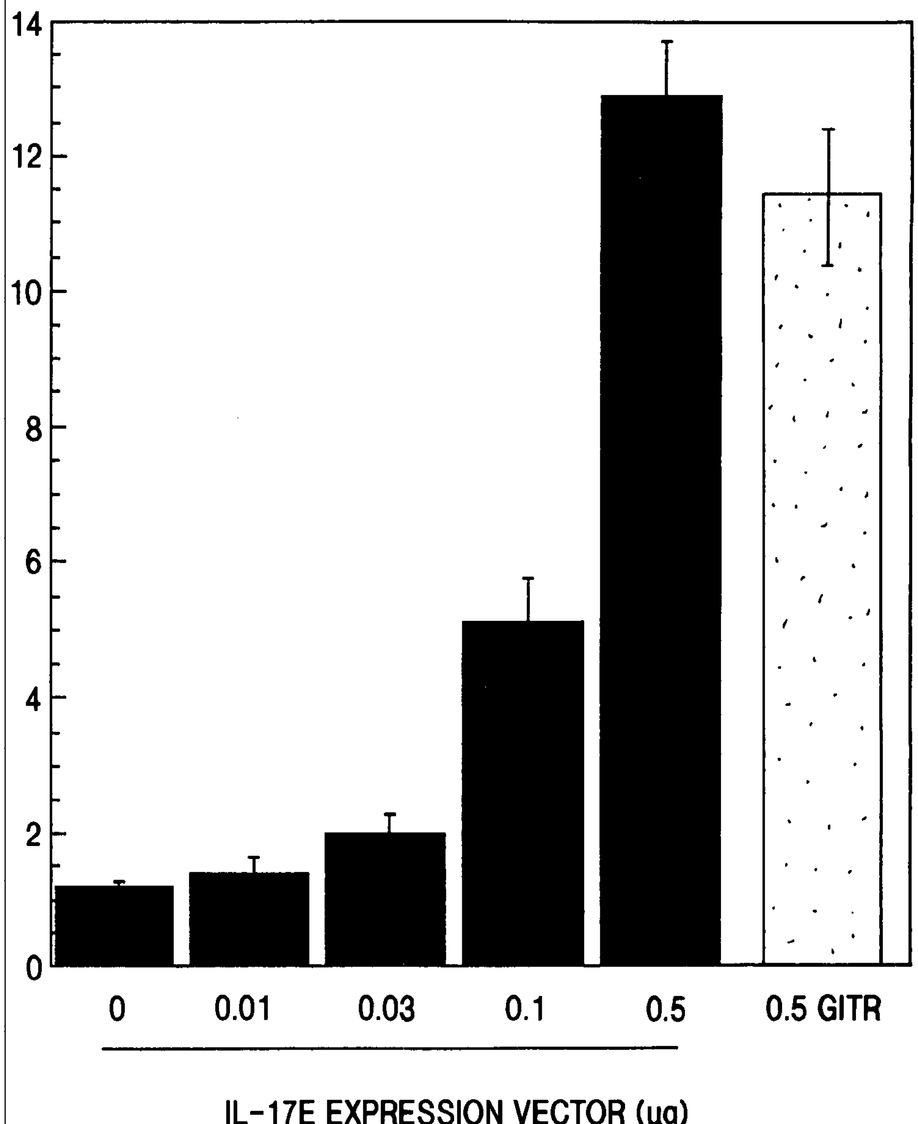


FIG. 33B

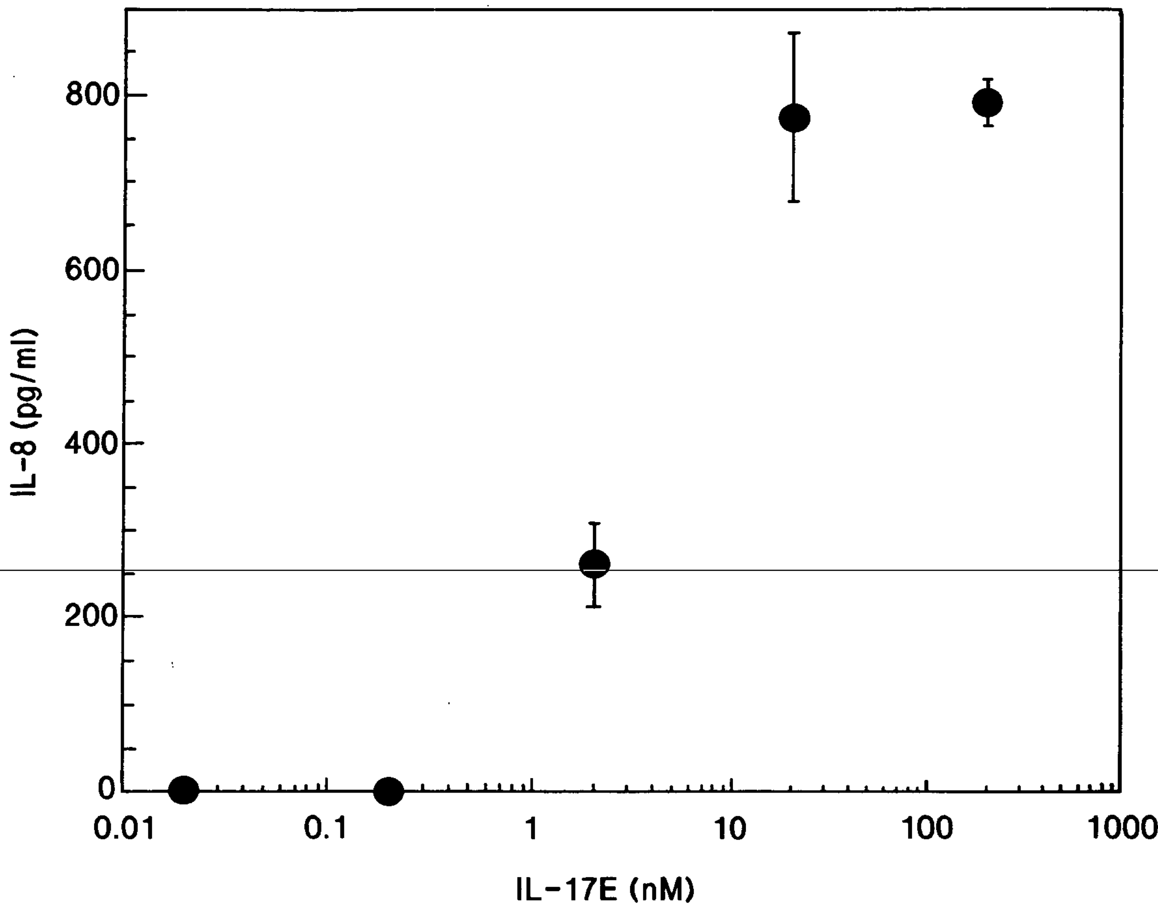


FIG. 34

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

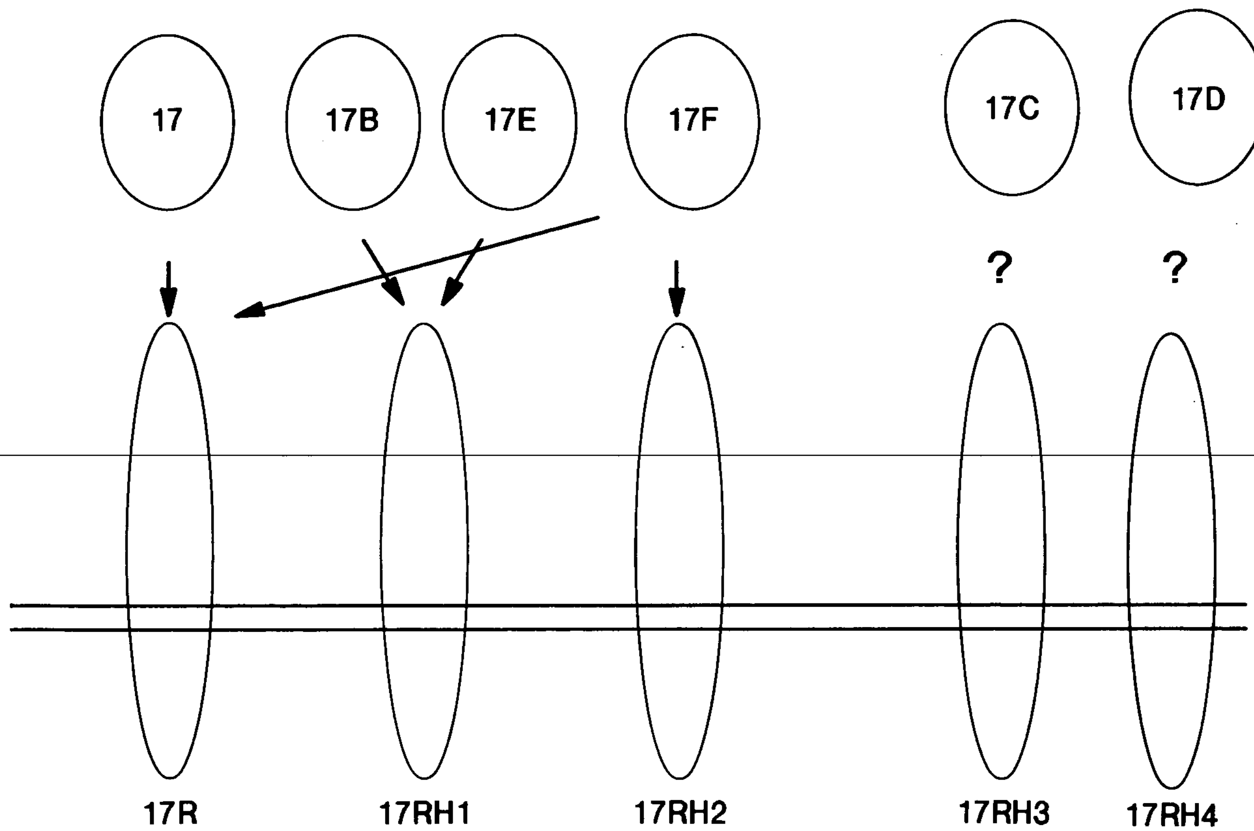


FIG. 35

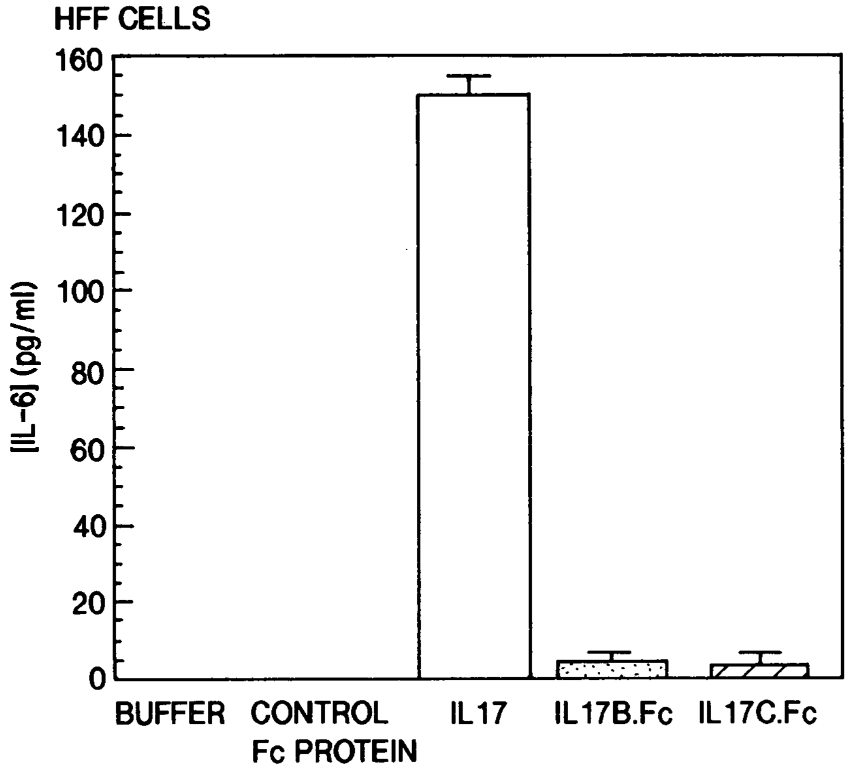


FIG. 36A

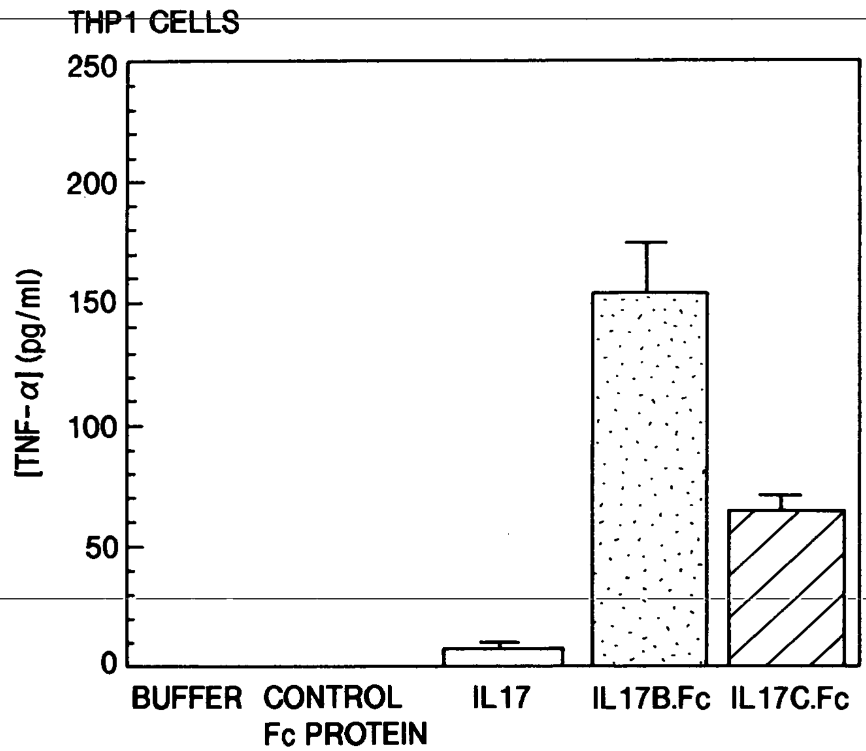


FIG. 36B

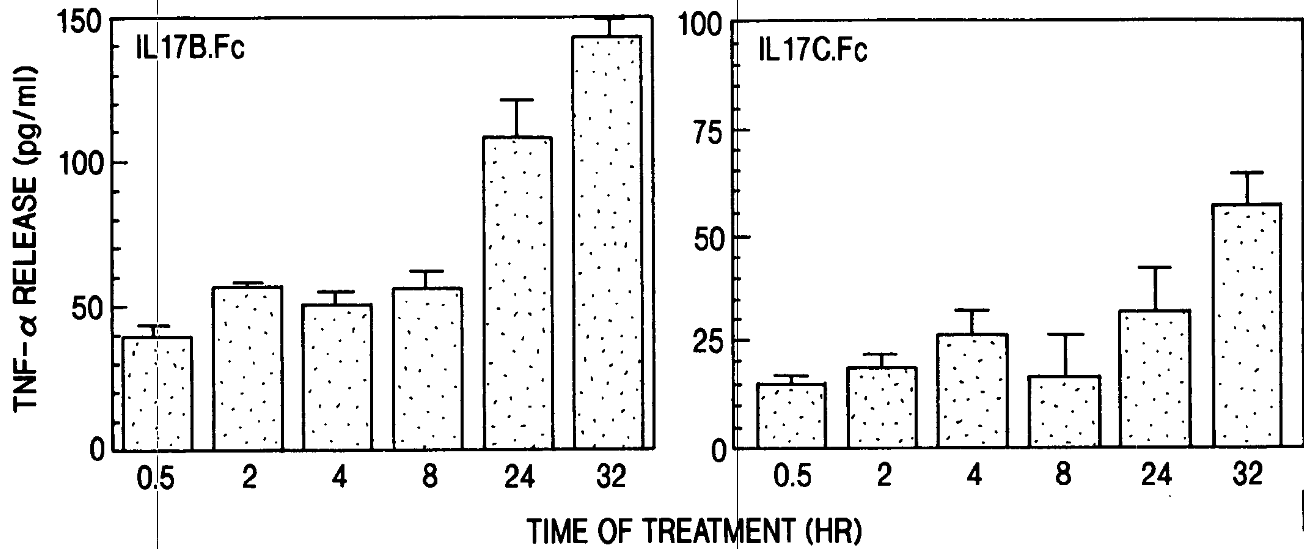


FIG. 37A

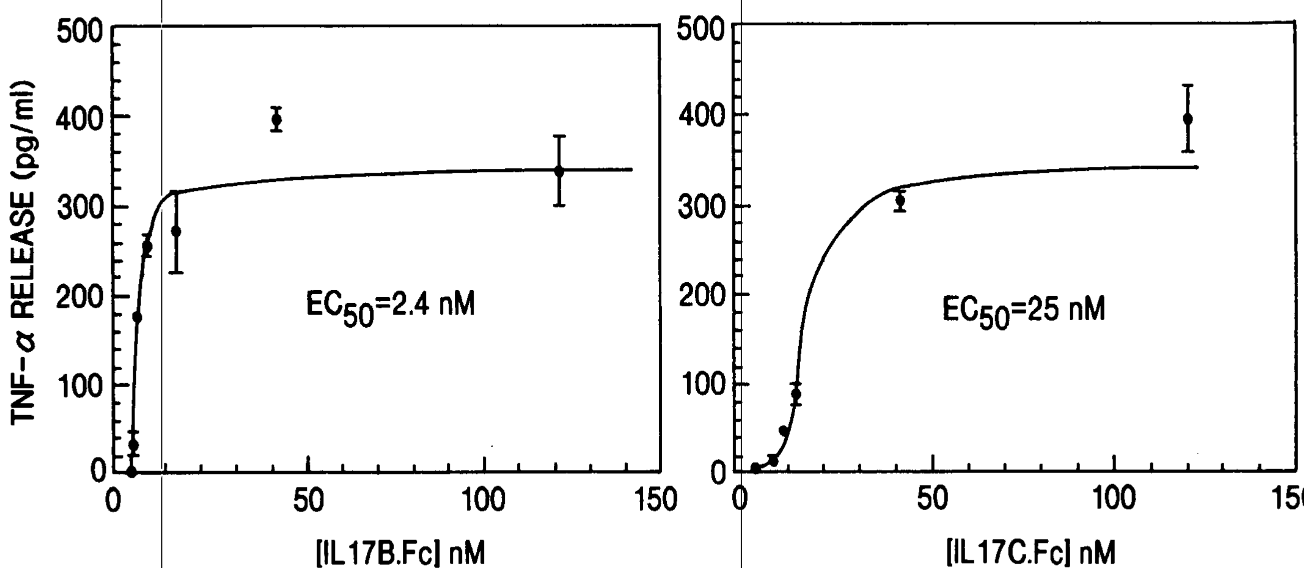


FIG. 37B

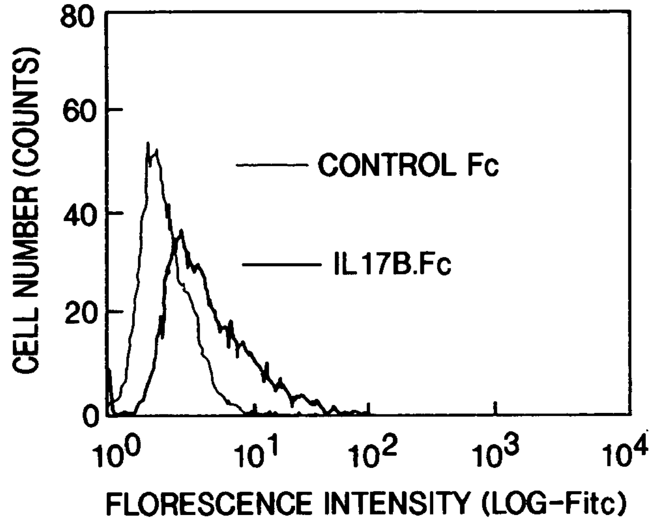


FIG. 38A

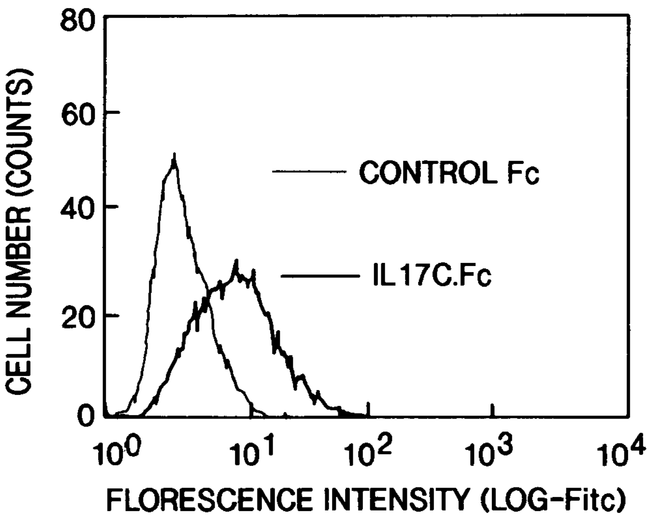


FIG. 38B

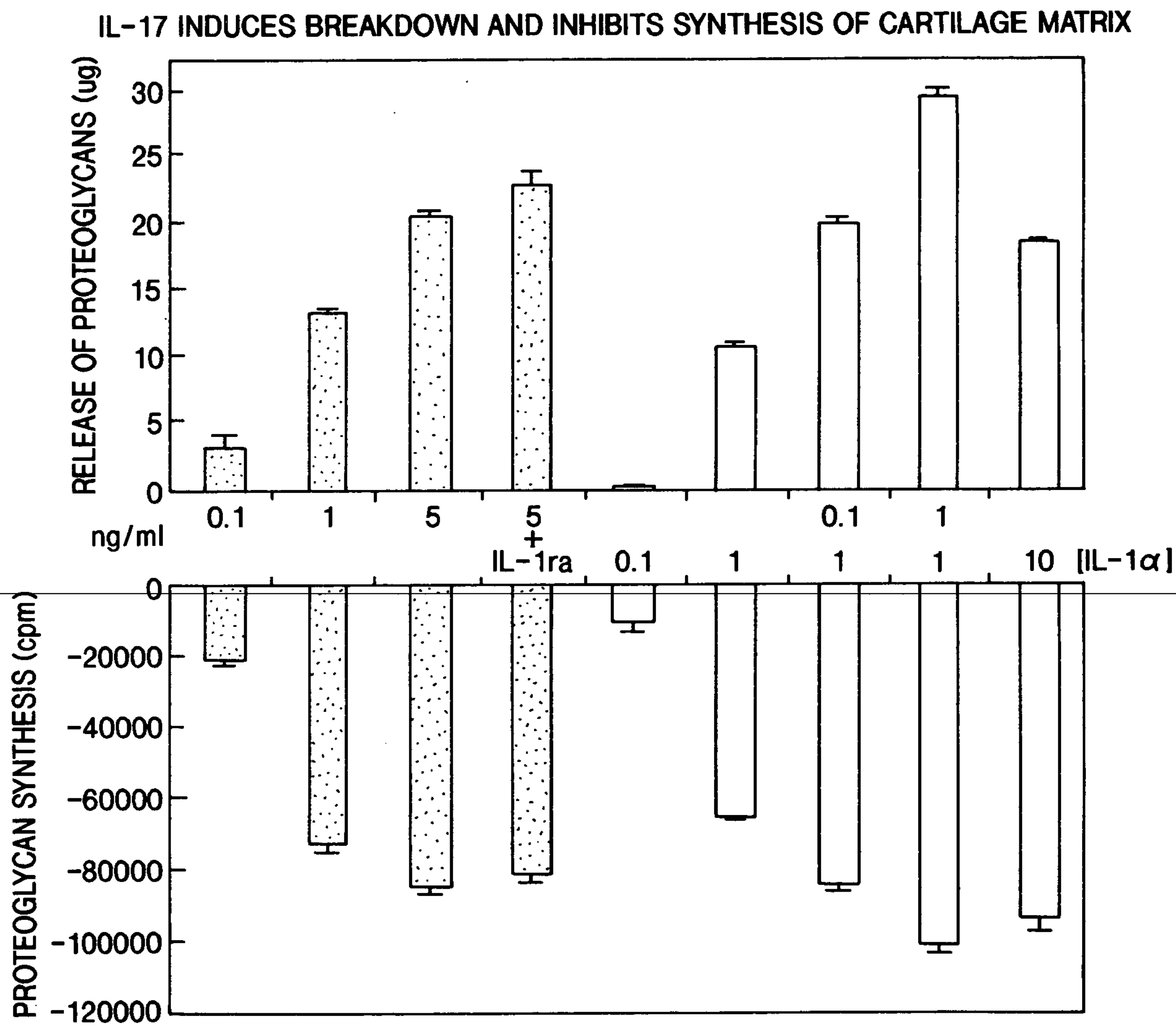
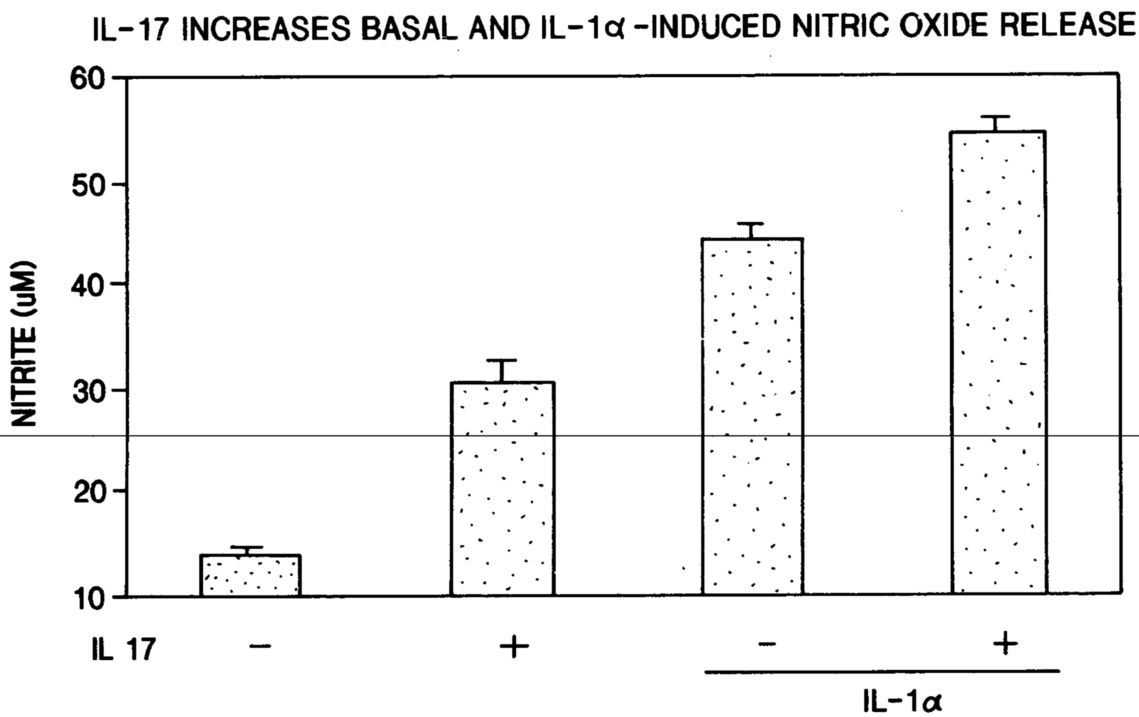

IL-17 INDUCES BREAKDOWN AND INHIBITS SYNTHESIS OF CARTILAGE MATRIX
RELEASE OF PROTEOGLYCANS (ug)
30
25
20
15
10
5
0
0.1
1
5
5
+
IL-1ra
0.1
1
ng/ml
0.1
1
1
1
10
[IL-1α]
0
-20000
-40000
-60000
-80000
-100000
-120000
PROTEOGLYCAN SYNTHESIS (cpm)

FIG. 39



IL-17 INCREASES BASAL AND IL-1α -INDUCED NITRIC OXIDE RELEASE
NITRITE (uM)
60
50
40
30
20
10
IL 17
−
+
−
+
IL-1α

FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

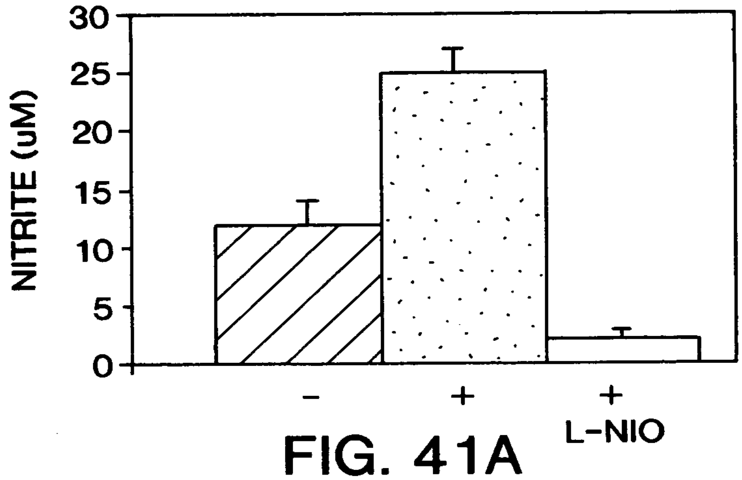


FIG. 41A

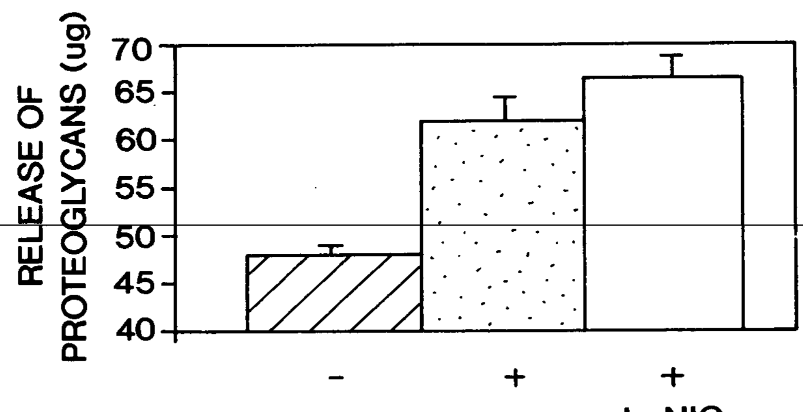


FIG. 41B

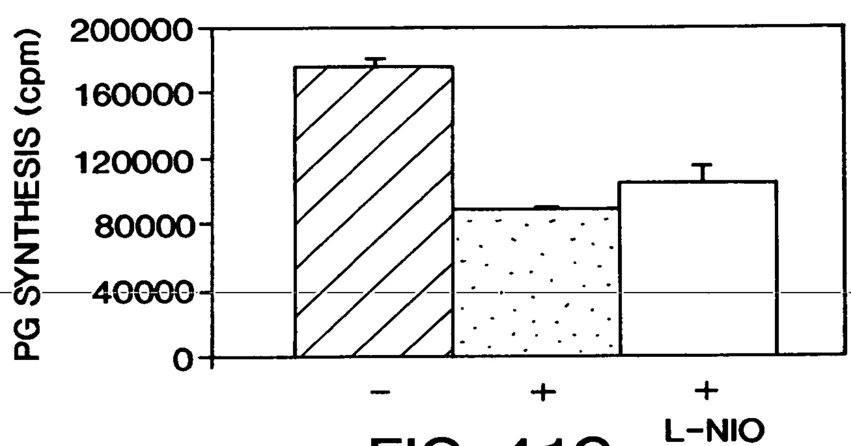


FIG. 41C

INHIBITION OF NO RELEASE ENHANCES IL1-α-INDUCED MATRIX BREAKDOWN BUT NOT MATRIX SYNTHESIS

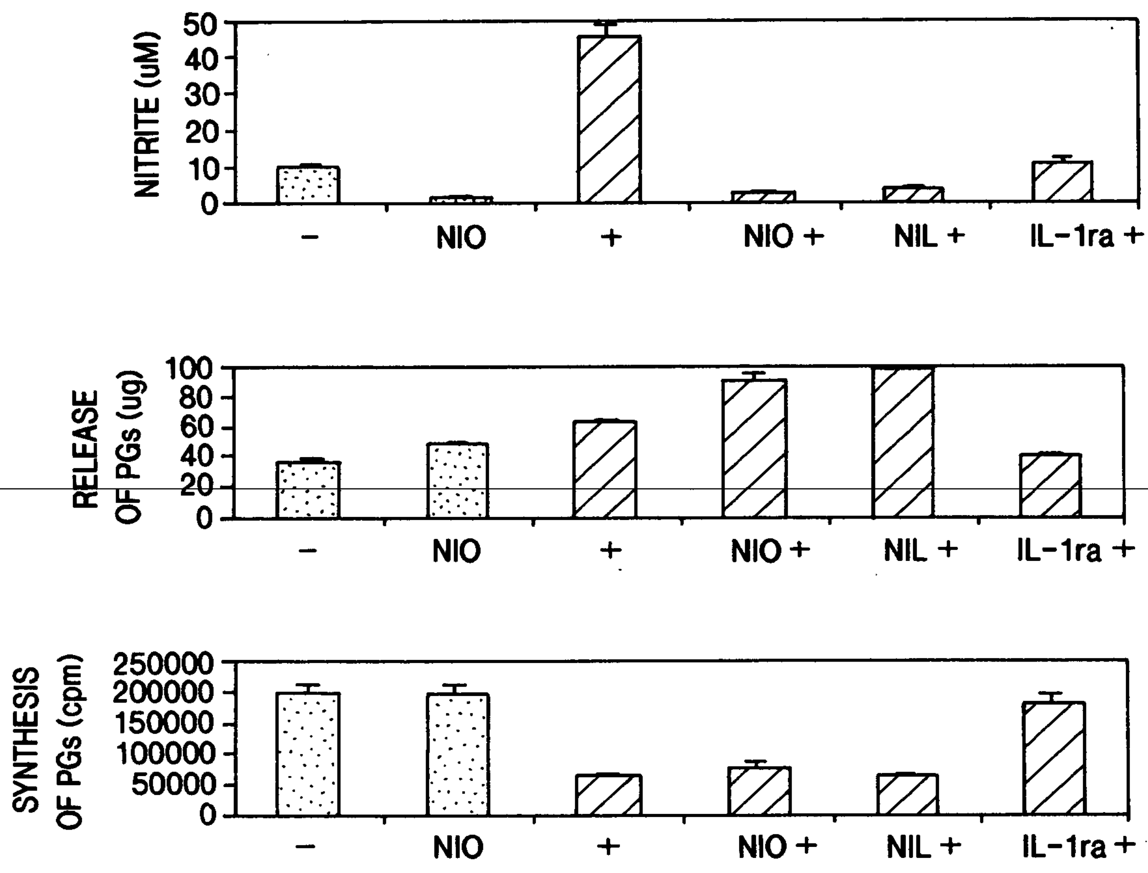


FIG. 42

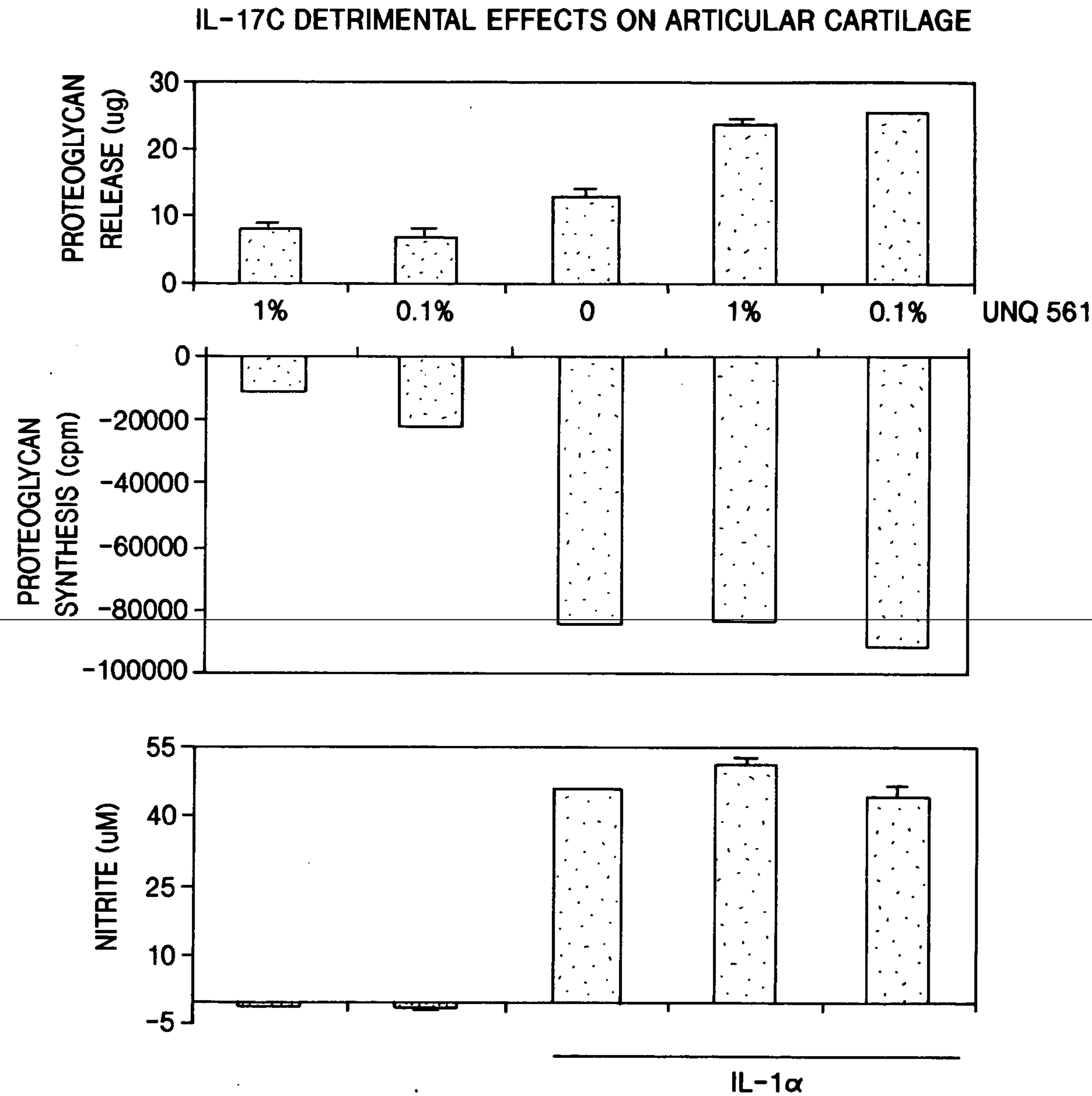

IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE
PROTEOGLYCAN RELEASE (ug)
30
20
10
0
1%
0.1%
0
1%
0.1%
UNQ 561
PROTEOGLYCAN SYNTHESIS (cpm)
0
-20000
-40000
-60000
-80000
-100000
NITRITE (uM)
55
40
25
10
-5
IL-1α

FIG. 43

INFLAMMATORY BOWEL DISEASE:
EXPRESSION OF IL-17 FAMILY IN MOUSE MODEL OF IBD

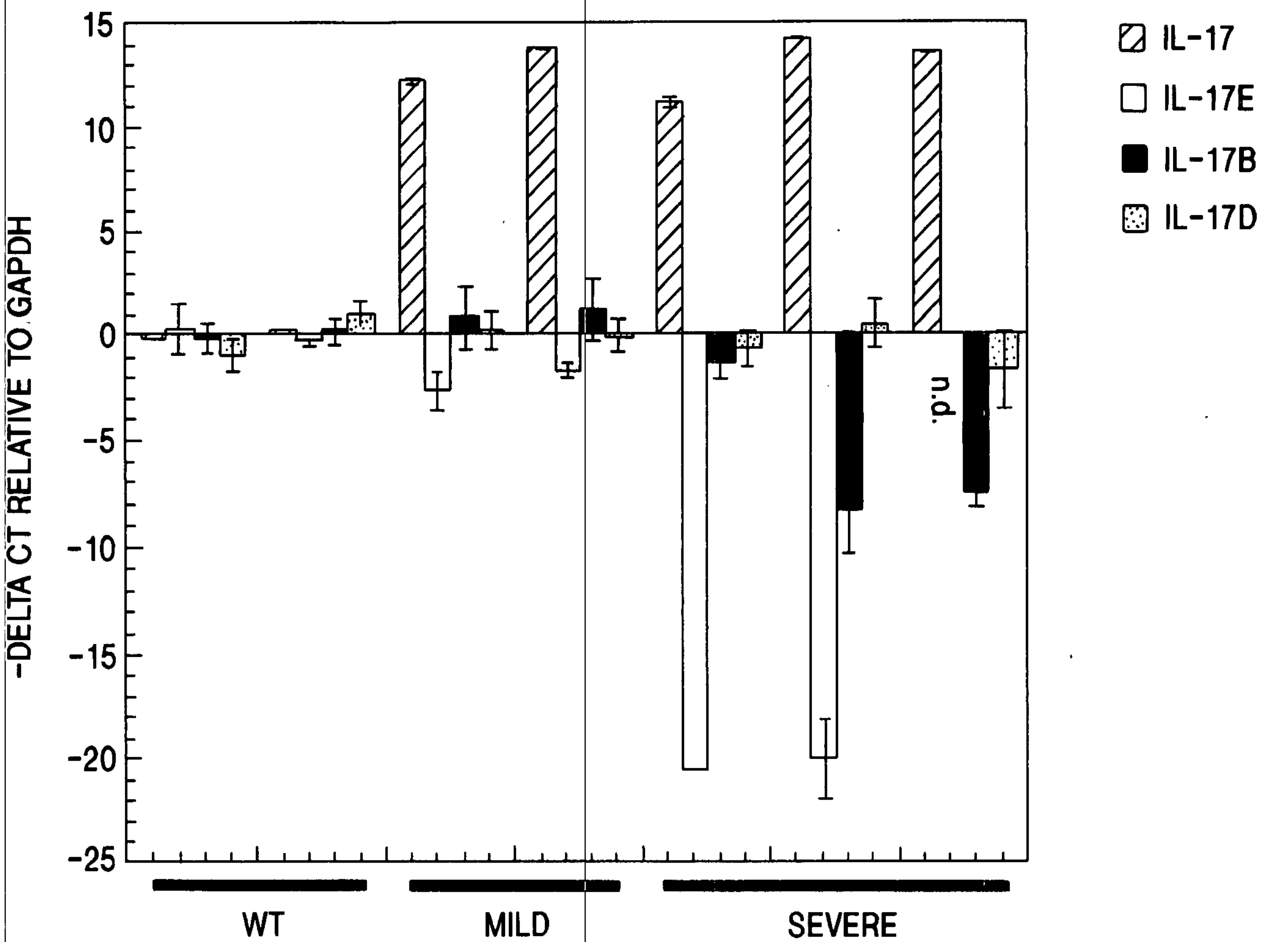


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

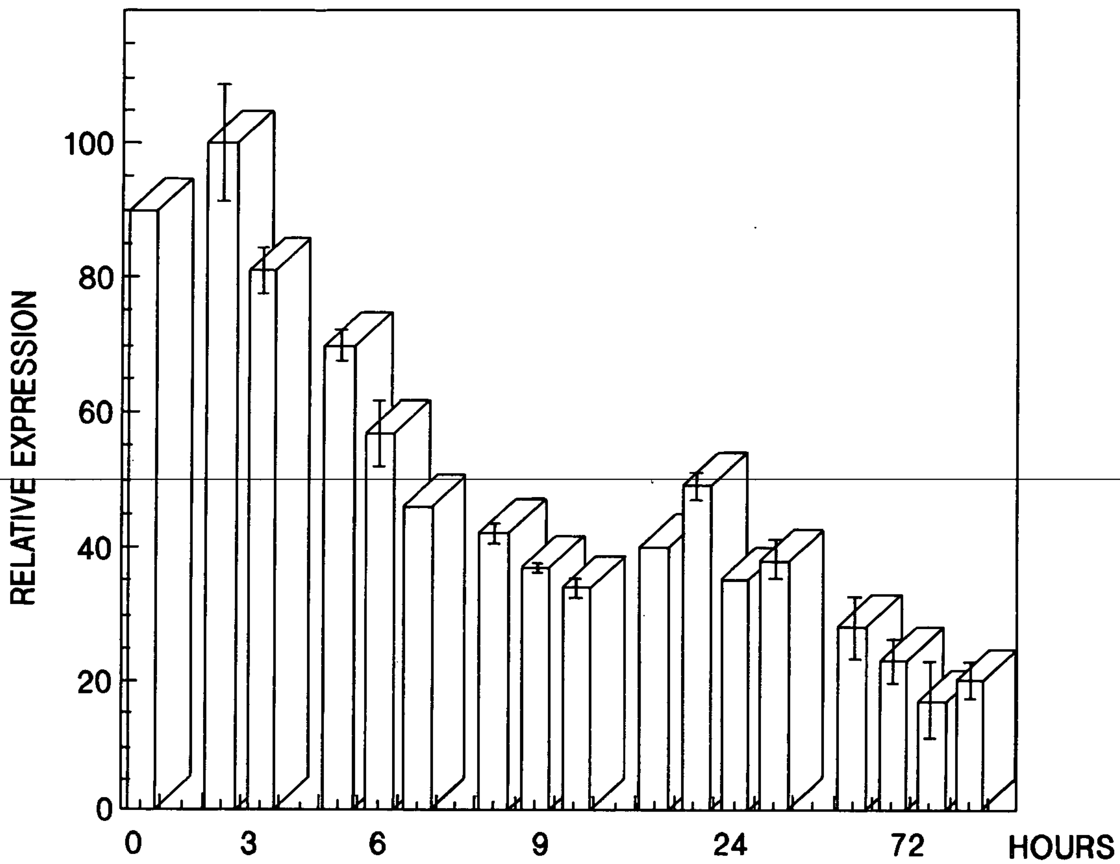


FIG. 45

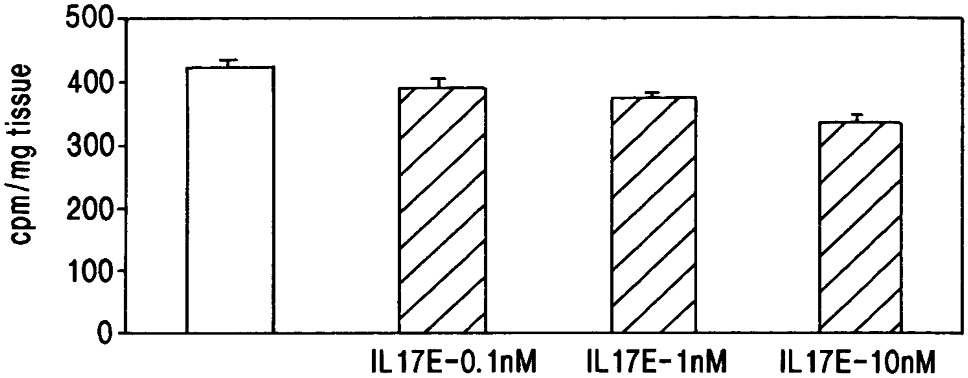


FIG. 46A

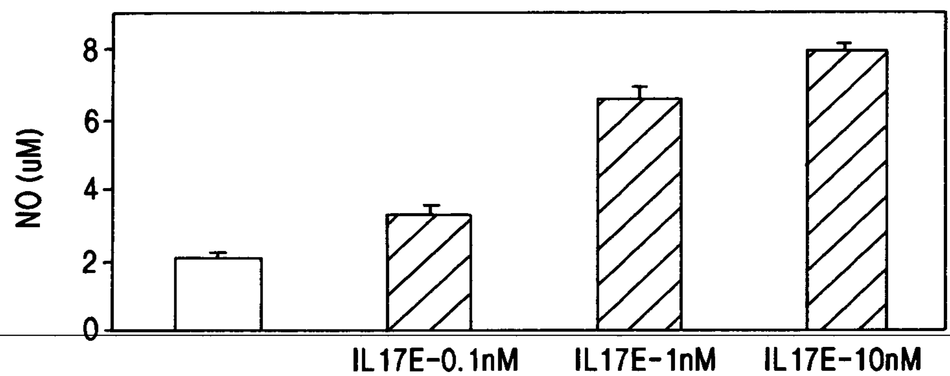


FIG. 46B

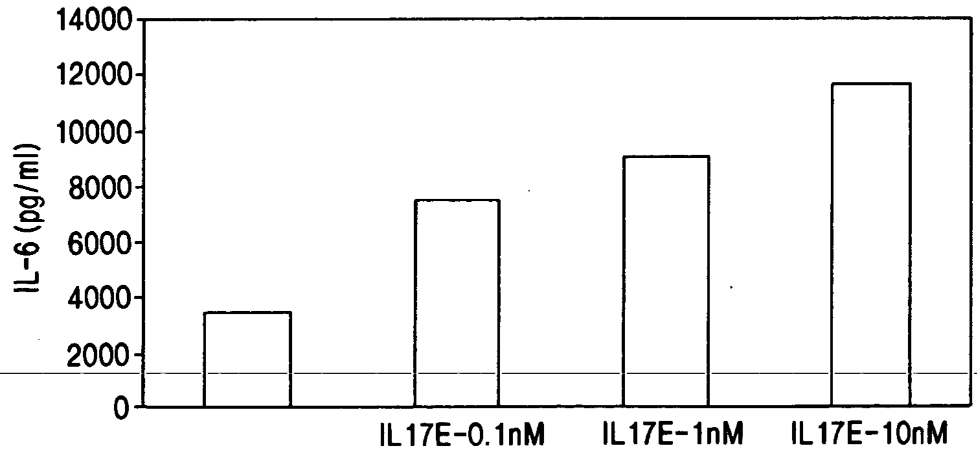


FIG. 46C

FIG. 47A

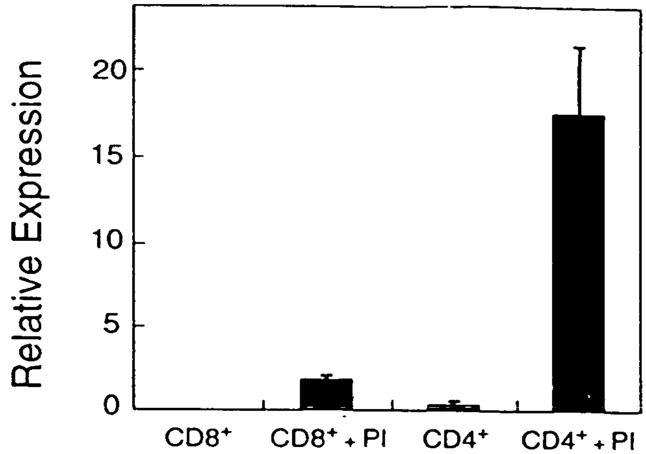


FIG. 47B

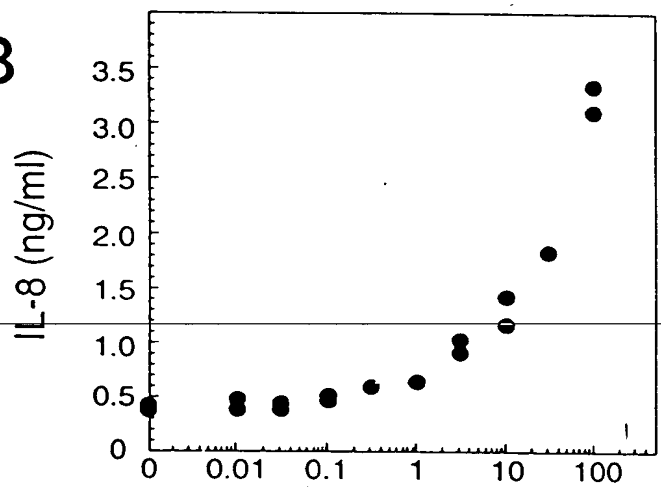
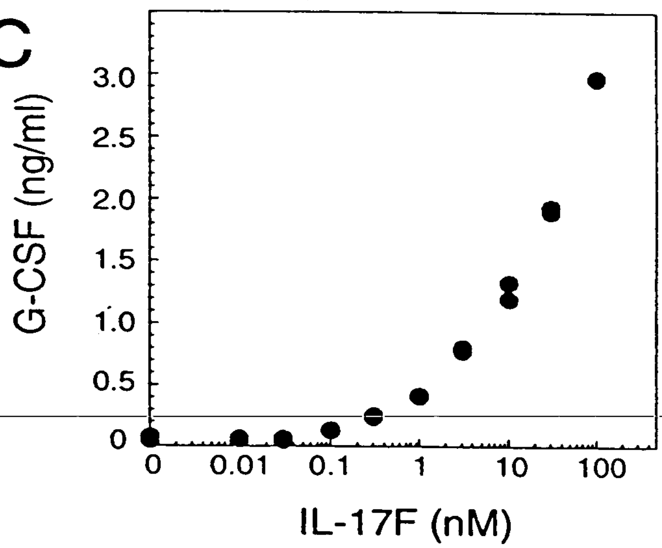


FIG. 47C



Porcine

Matrix Breakdown

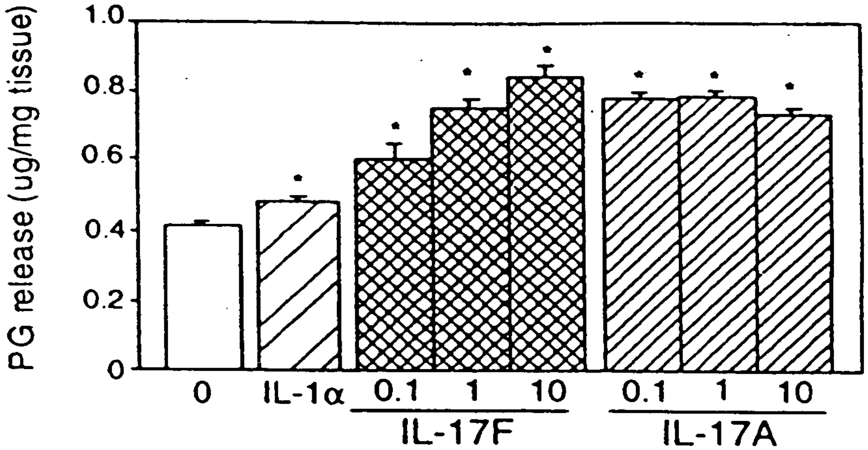


FIG. 48A

Matrix Synthesis

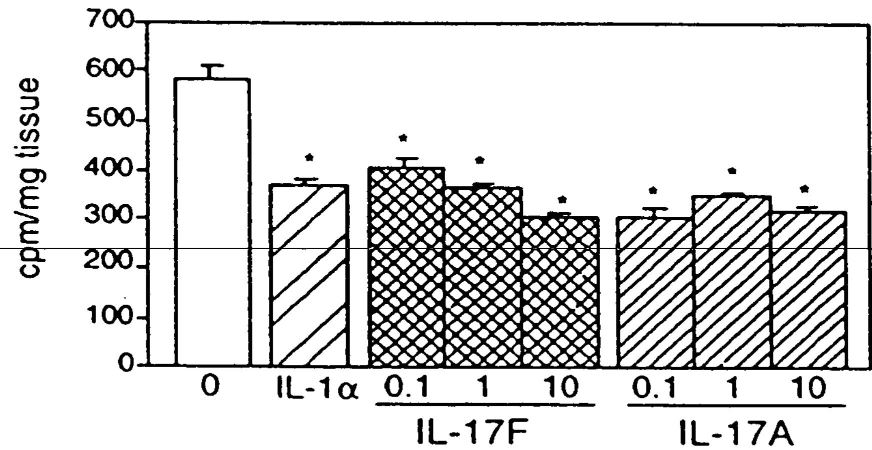


FIG. 48B

IL-6 production

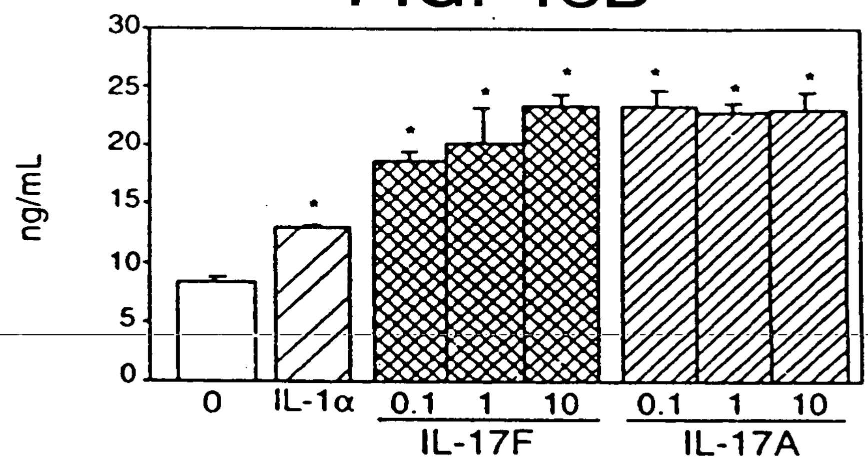


FIG. 48C

Human

Matrix Breakdown

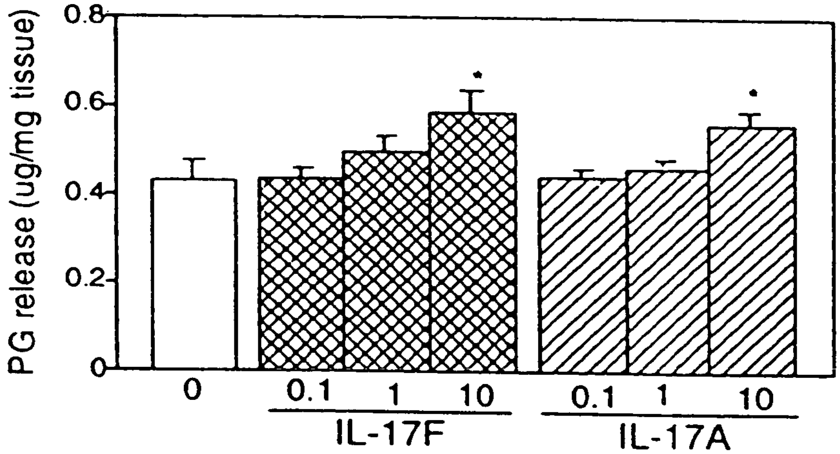


FIG. 48D

Matrix Synthesis

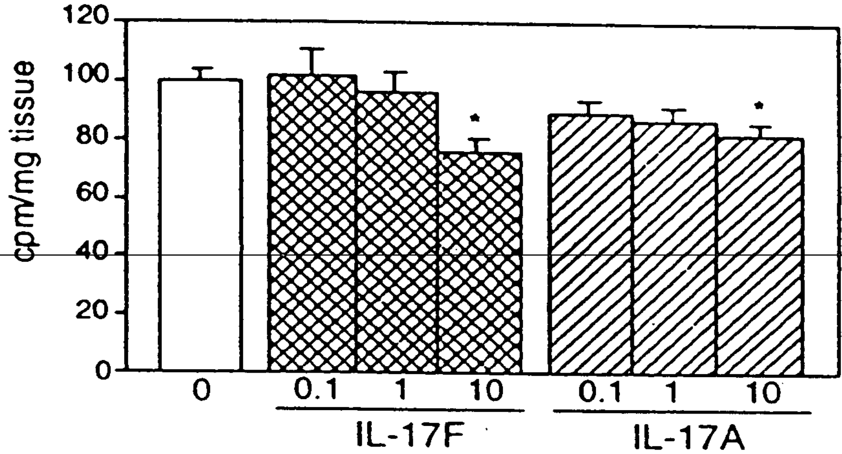


FIG. 48E

IL-6 production

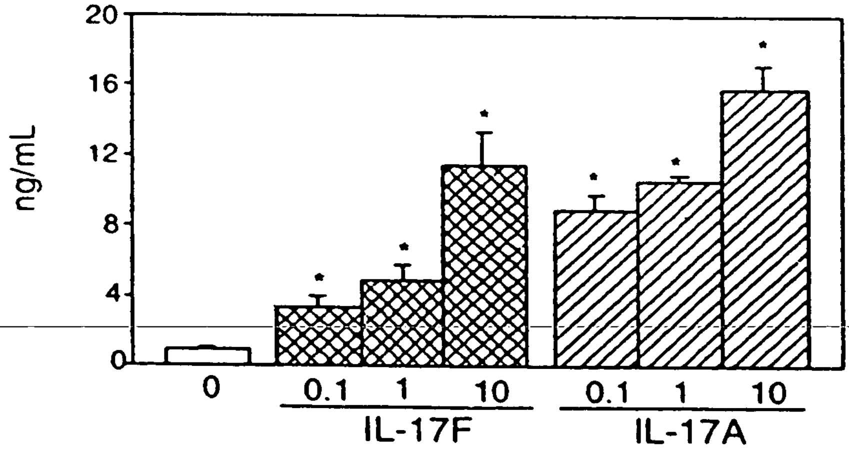


FIG. 48F

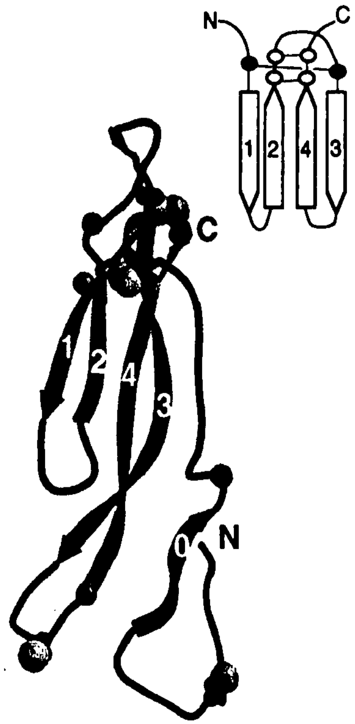


FIG. 49A

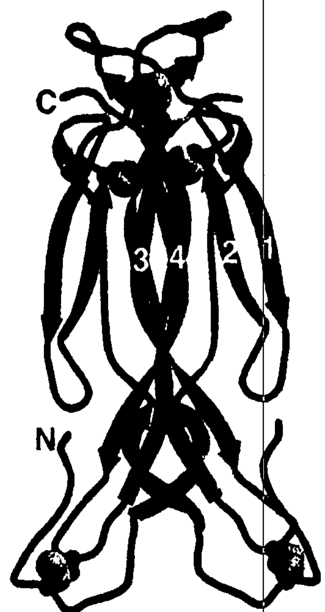


FIG. 49B

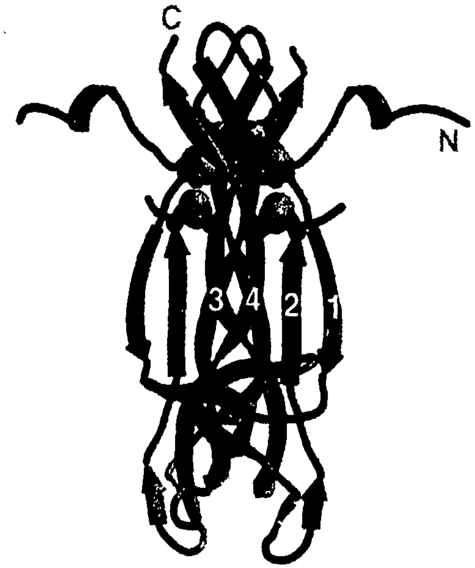


FIG. 49C

					*	
IL-17F	....	....	....	...RKIPKVG	HTFFQKPESC	17
IL-17A	....	....	....	.....IVKAG	ITIPRNP.GC	14
IL-17B	......QPRS	PKSKRKGQGR	PGPLAPGPHQ	VPLDLVSRMK	PYARMEEYER	44
IL-17C	HHDPSLRGHP	HSHGTPHCYS	AEELPLGQAP	PHLLARGAKW	GQALPVALVS	50
IL-17E	....	....	........YS	HWPSCCPSKG	QDTSEELLRW	22

		0			1	
IL-17F	PPVPGG....	....SMKLDI	GIINENQRVS	MSRNIESRST	CPWNYTVTWD	59
IL-17A	PNSEDKNFPR	TVMVNLNIHN	RNTNTN..PK	RSSDYYNRST	CPWNLHRNED	62
IL-17B	NIEEMVAQLR	..NSSELAQR	KCEV....NL	QLWMSNKRSL	CPWGYSINHD	88
IL-17C	SLEAASHRGR	..HERPSATT	QCPVLRPEEV	LEADTHQRSI	CPWRYRVDTD	98
IL-17E	STVPVPPLEP	..ARPNRHPE	SCRASE....	.DGPLNSRAI	CPWRYELDRD	65

		2		3		
IL-17F	PNRYPSEVVQ	AQCRNLGCIN	A..QGKEDIS	MNSVPI.QQE	TLVVRRKHQG	106
IL-17A	PERYPSVIWE	AKCRHLGCIN	A..DGNVDYH	MNSVPI.QQE	ILVLRREPPH	109
IL-17B	PSRIPVDLPE	ARCLCLGCVN	PF.TMQEDRS	MVSVPV.FSQ	VPVRRR...L	133
IL-17C	EDRYPQKLAF	AECLCRGCID	AR.TGRETAA	LNSVRL.LQS	LLVLRR..RP	144
IL-17E	LNRLPQDLYH	ARCLCPHCVS	LQTGSHMDPR	GNSELLYHNQ	TVFYRRP...	112

	*			4		
IL-17F	CSV.......	....SFQLEK	VL..VTVGCT	CVTPVIHHVQ	...	133
IL-17A	CPN.......	....SFRLEK	IL..VSVGCT	CVTPIVHHVA	...	136
IL-17B	CPPPPRTGP.	.....CRQRA	VMETIAVGCT	CIF.......	...	160
IL-17C	CSRDGSGLPT	PGAFAFHTEF	IH..VPVGCT	CV.LPRSVAA	ALE	184
IL-17E	CHGEKGTHKG	.....YCLER	RLYRVSLACV	CVRPRVMG..	...	145

FIG. 50

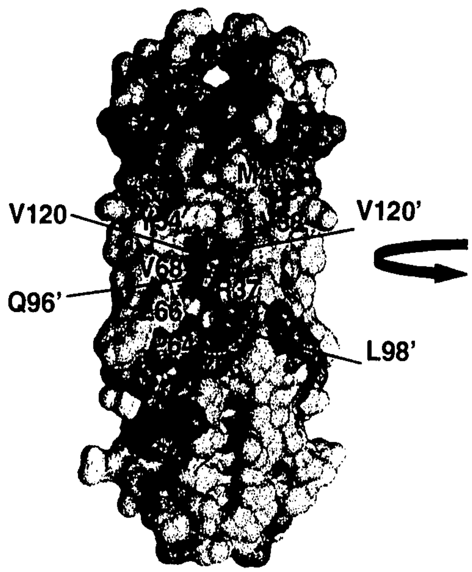


FIG. 51A

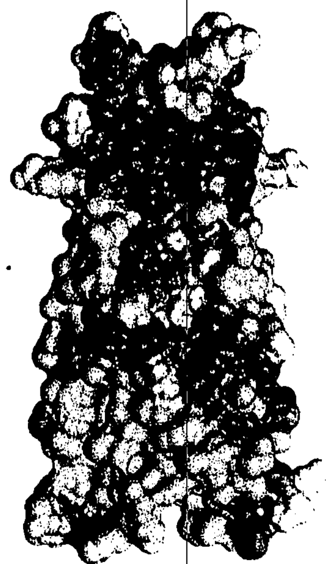


FIG. 51B

FIG. 51C

FIG. 52A

FIG. 52B

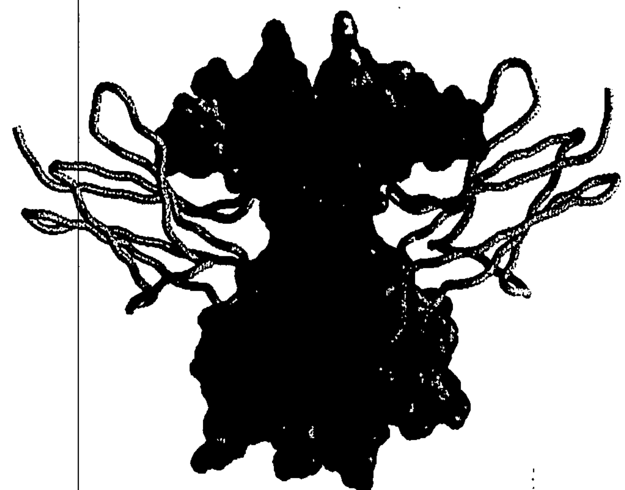


FIG. 52C

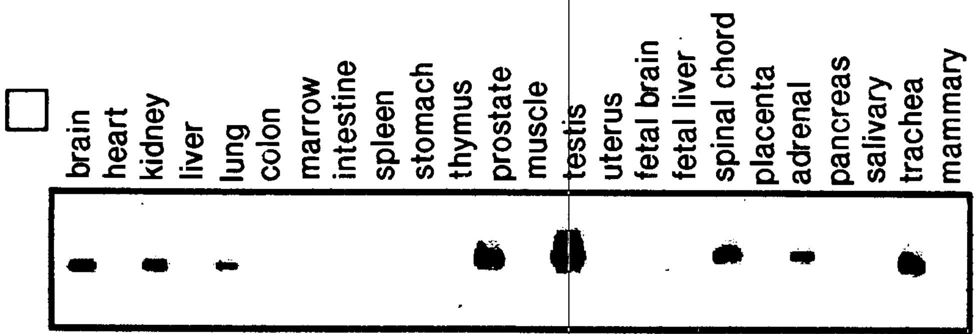
IL-17E is highly conserved between human and mouse

```
mIL-17E    1  --------------------VAFLAMIVGTHTVSLRIQEGCSHLPSCCPS
hIL-17E    1  MRERPRLGEDSSLISLFLQVVAFLAMVMGTHT--------YSHWPSCCPS

mIL-17E   35  KEQEPPEEWLKWSSASVSPPEPLSHTHHAESCRASKDGPLNSRAISPWSY
hIL-17E   43  KGQDTSEELLRWSTVPVPPLEPARPNRHPESCRASEDGPLNSRAISPWRY

mIL-17E   85  ELDRDLNRVPQDLYHARCLCPHCVSLQTGSHMDPLGNSVPLYHNQTVFYR
hIL-17E   93  ELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR

mIL-17E  135  RPCHGEEGTHRRYCLERRLYRVSLACVCVRPRVMA
hIL-17E  143  RPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG
```

FIG. 53

Tissue distribution of IL-17E

Human

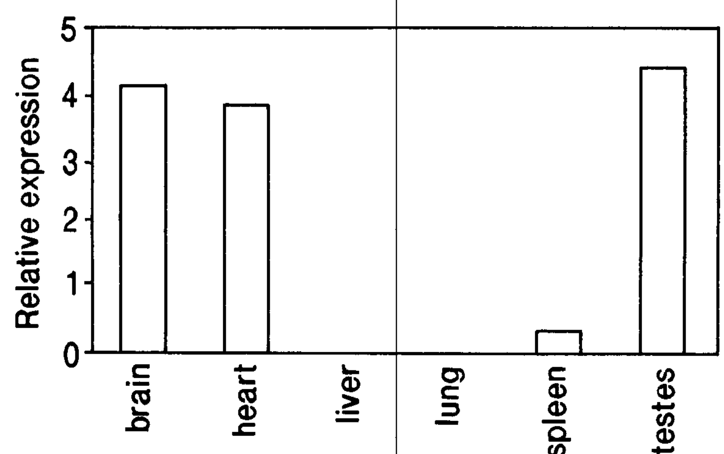


IL-17E is not induced
in activated T cells

IL-17E (PCR then probed with cDNA)

FIG. 54B

Mouse



Taqman assay

FIG. 54A

mIL-17E transgenics are growth retarded

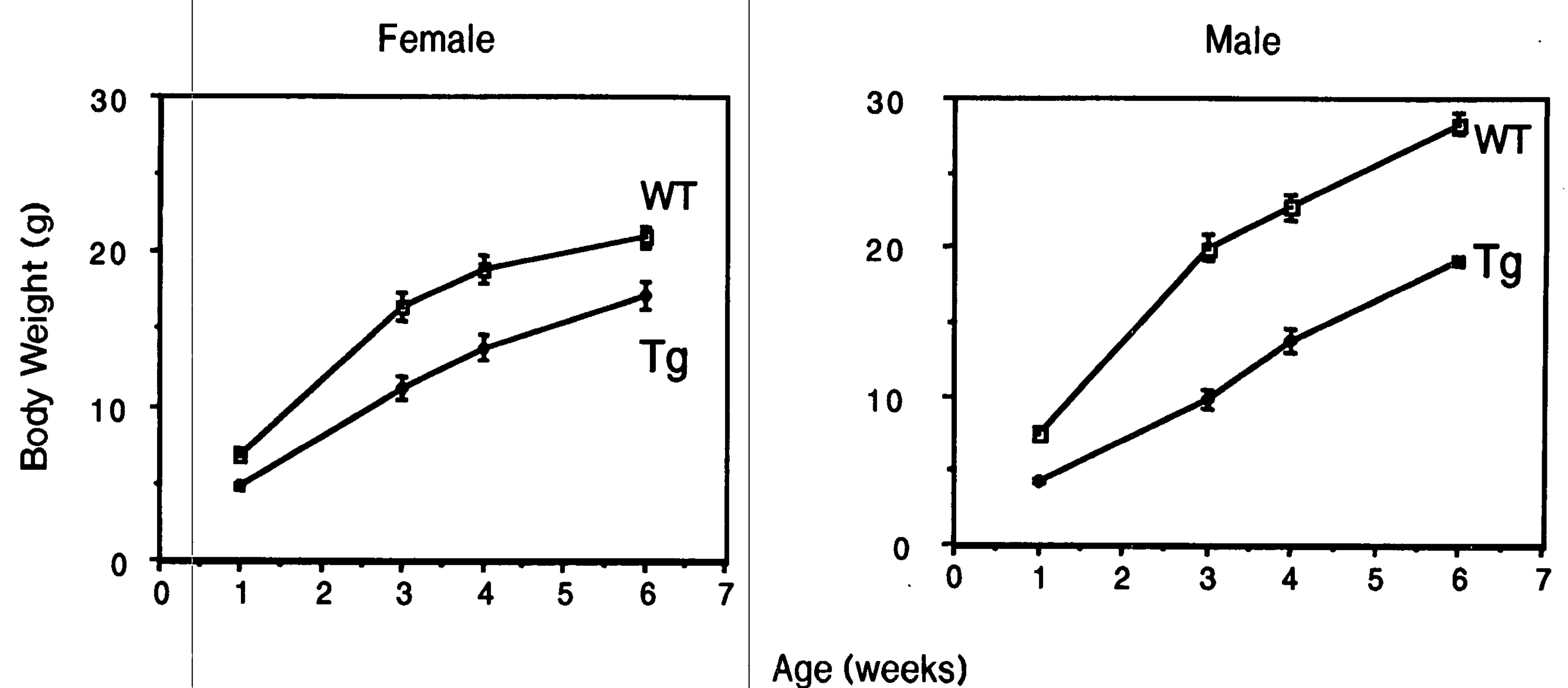


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age

TG

WT

FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

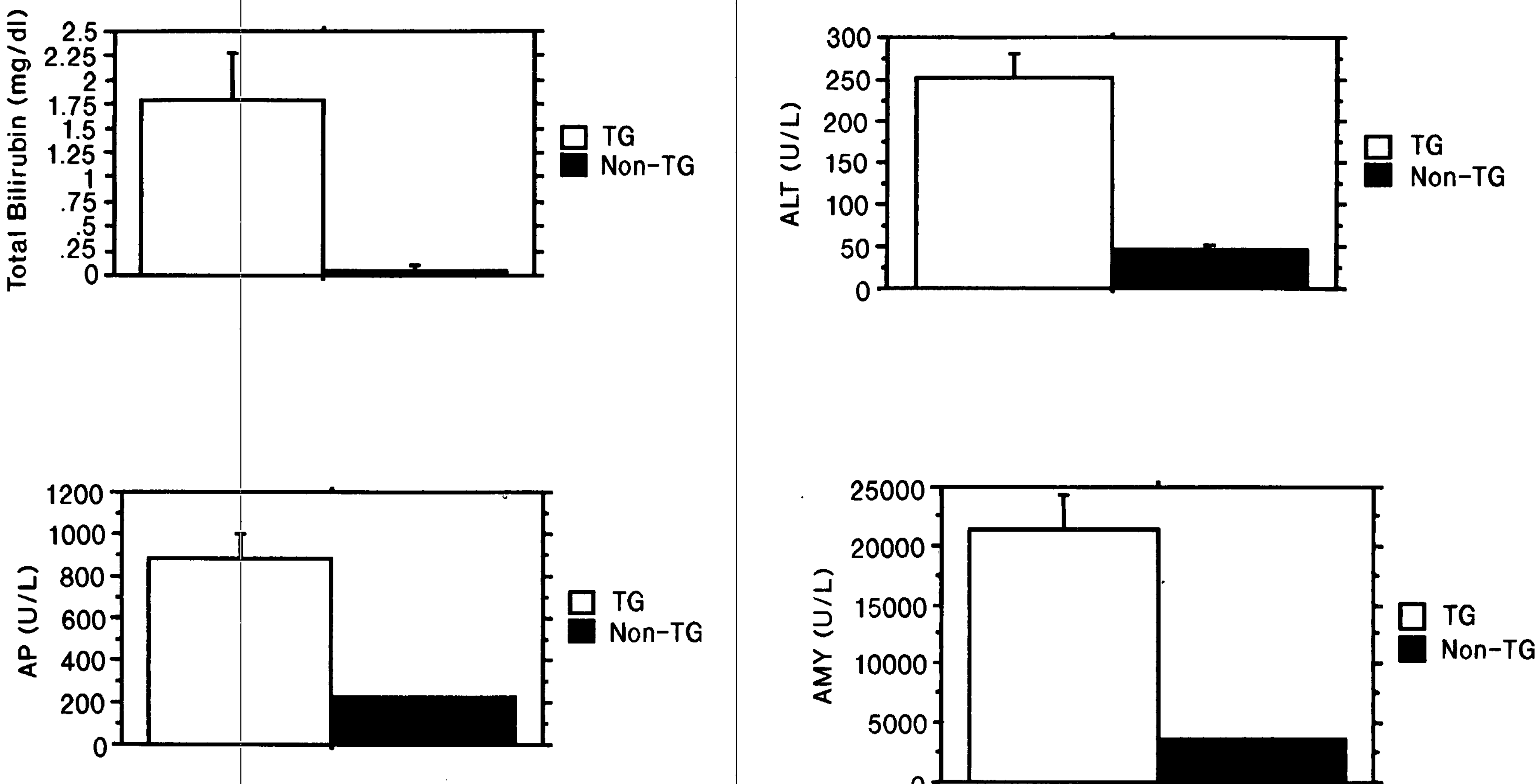


FIG. 57

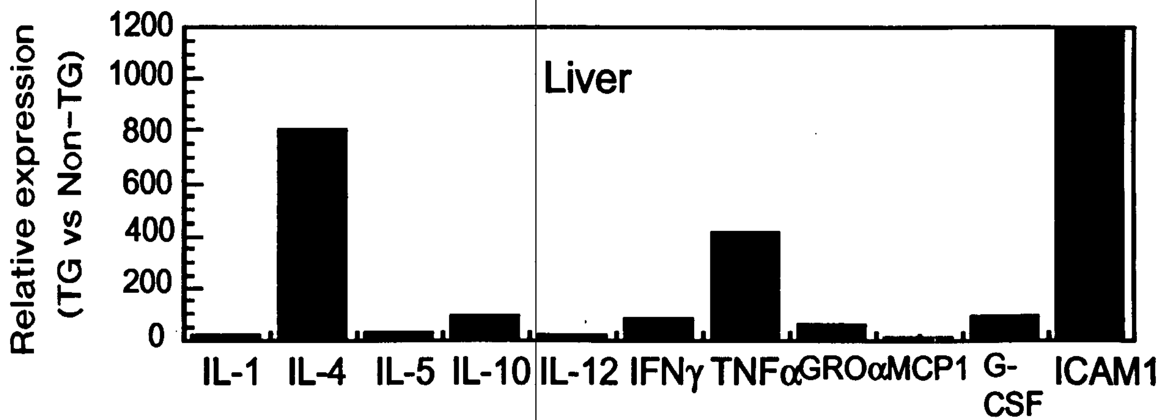

Relative expression
(TG vs Non-TG)
1200
1000
800
600
400
200
0
Liver
IL-1
IL-4
IL-5
IL-10
IL-12
IFNγ
TNFα
GROα
MCP1
G-
CSF
ICAM1

FIG. 58A

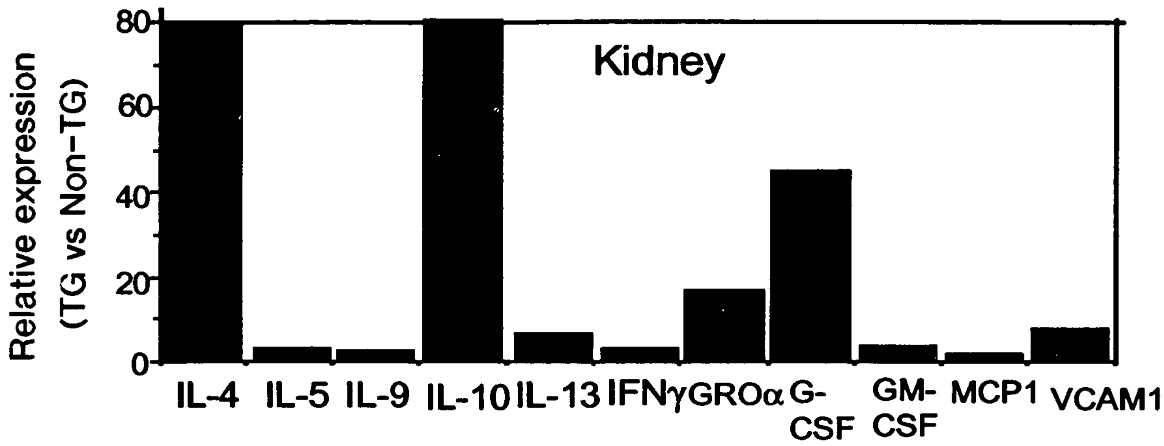


FIG. 58B

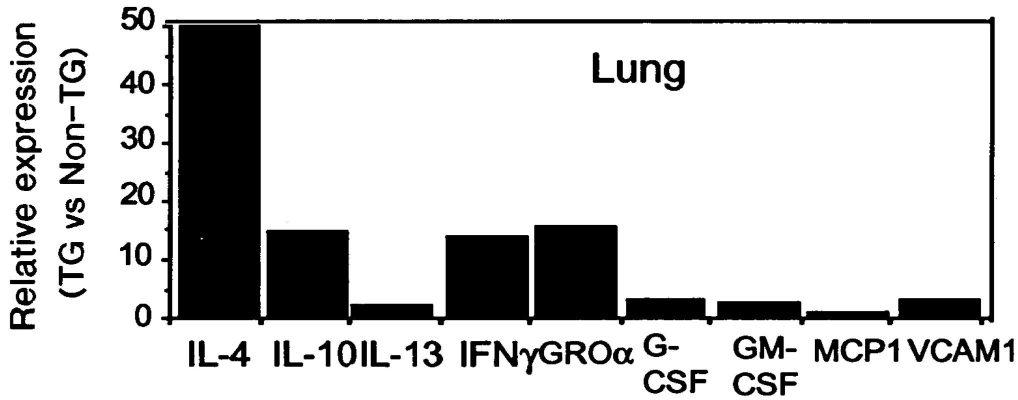


FIG. 58C

Gene profiling of IL-17E transgenics (Taqman)

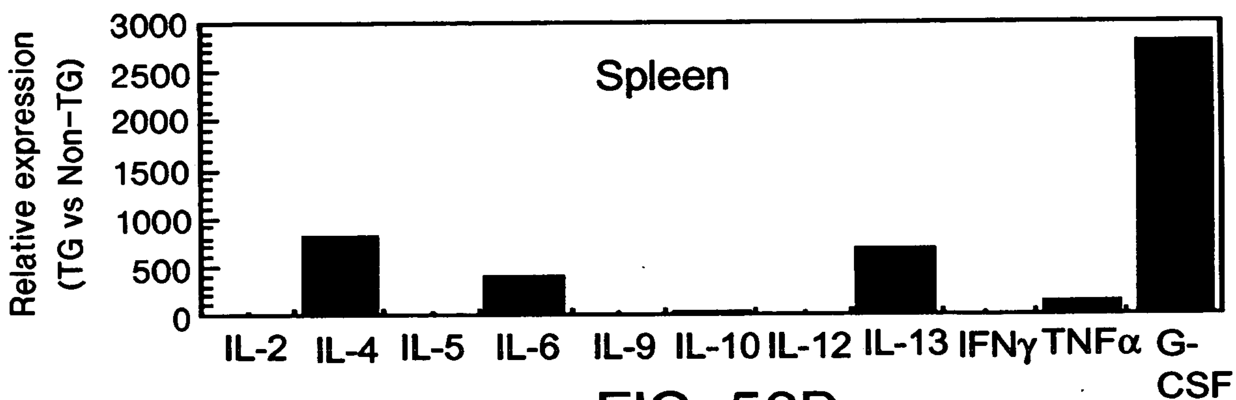


FIG. 58D

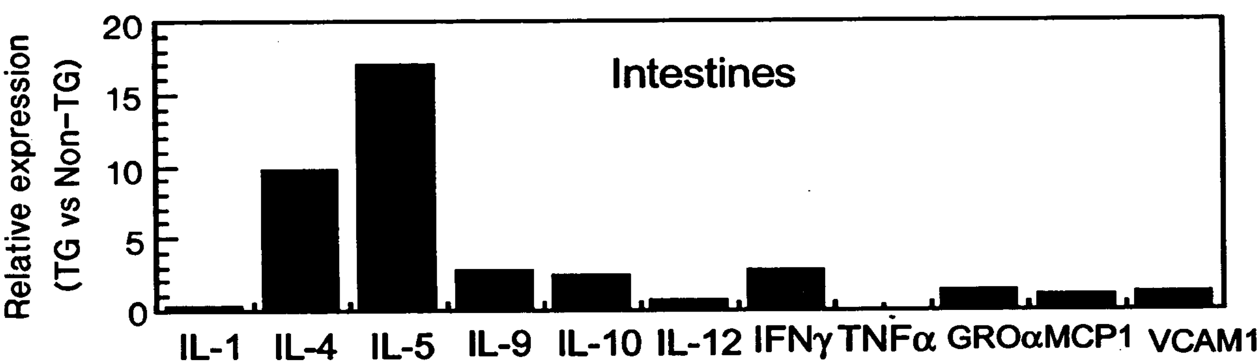
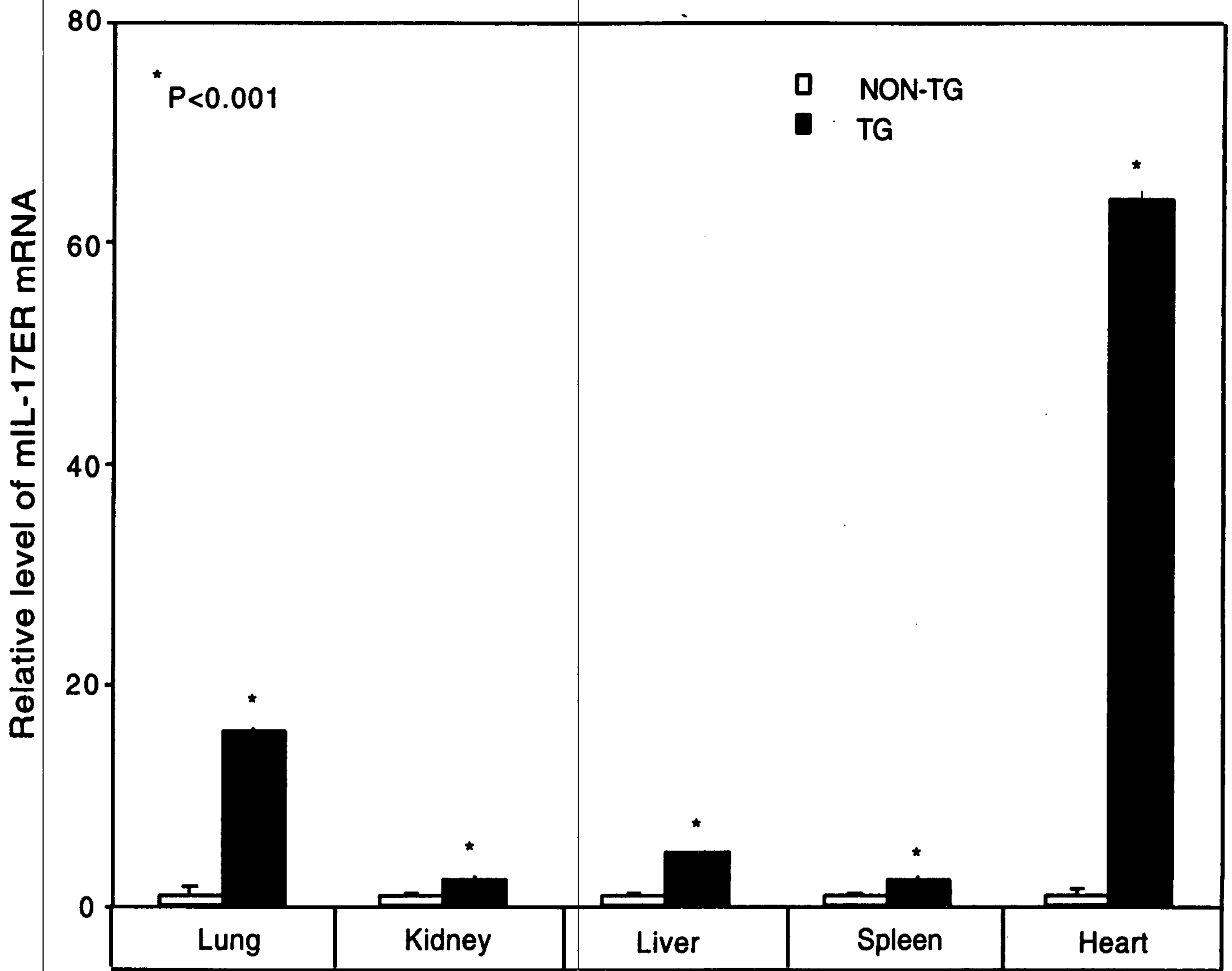


FIG. 58E



Relative level of mIL-17ER mRNA
80
60
40
20
0
* P<0.001
NON-TG
TG
Lung
Kidney
Liver
Spleen
Heart

FIG. 59

Elevated serum IL−5, IL−13 and TNF α in mIL−17E transgenics

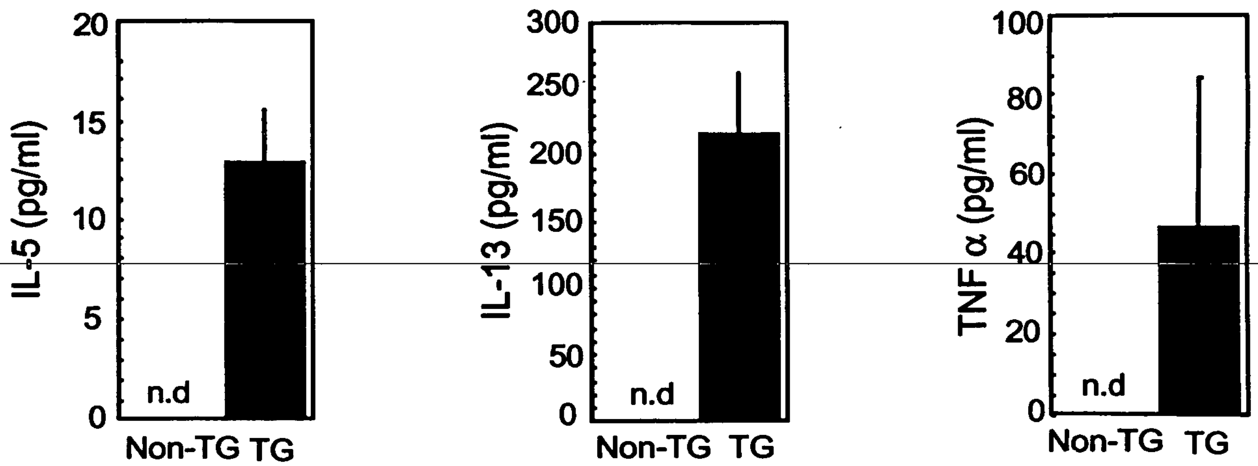


FIG. 60

Serum IgE and IgG1, but not IgG2a is elevated in mIL-17E transgenics

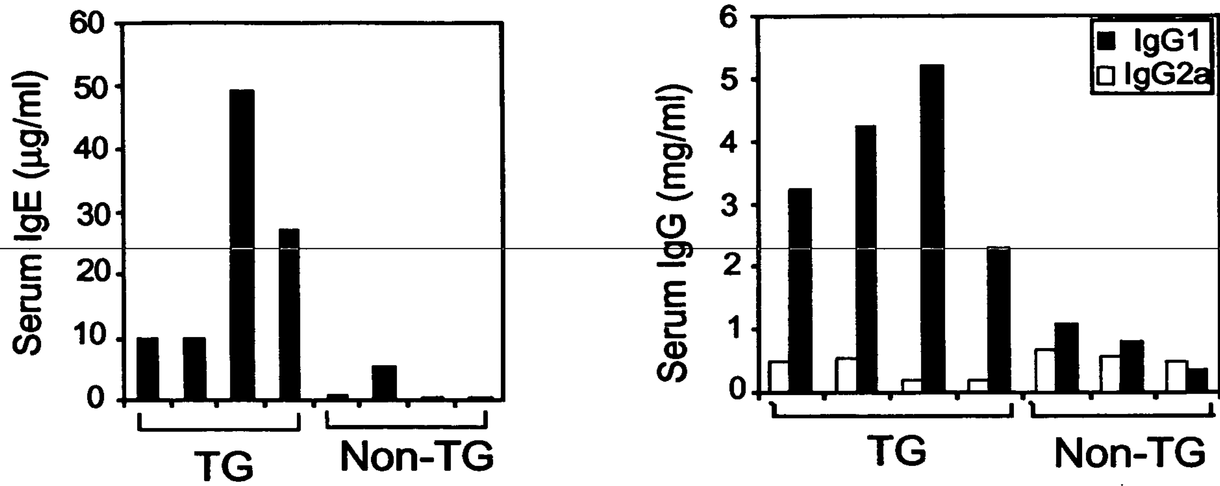


FIG. 61

Neutrophilia in mIL-17E transgenics
(8 wks, PBMC by FACS)

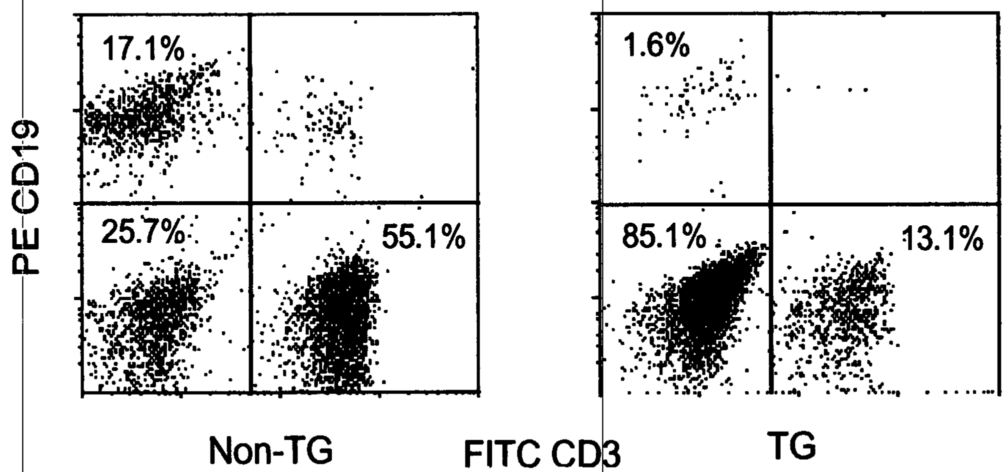


FIG. 62A

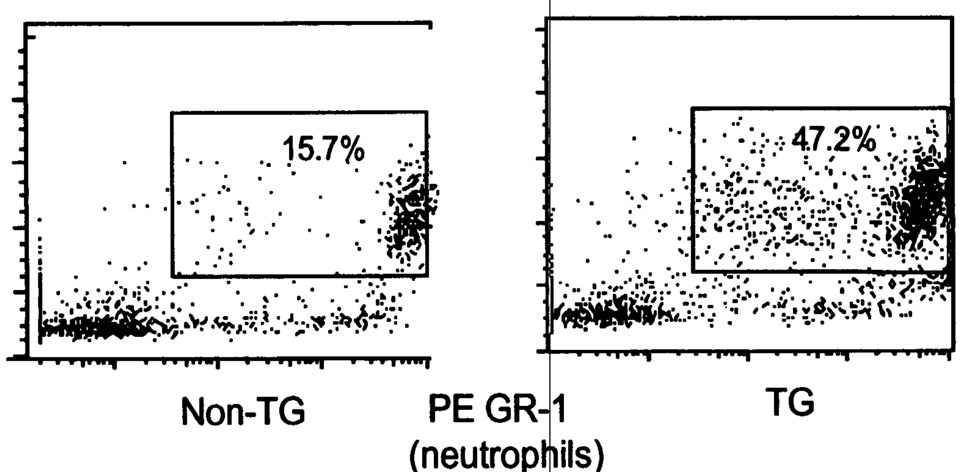


FIG. 62B

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

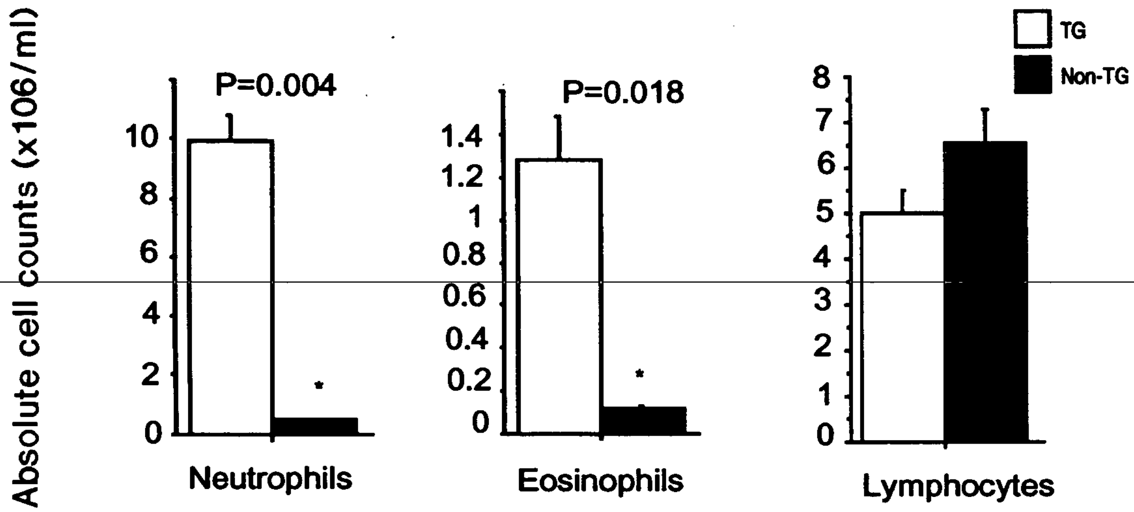


FIG. 63

G–CSF is elevated in
mIL–17E transgenics

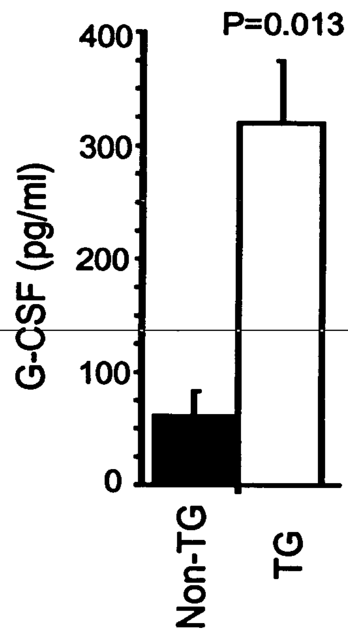


FIG. 64

IL-17E induces production of G-CSF in vitro

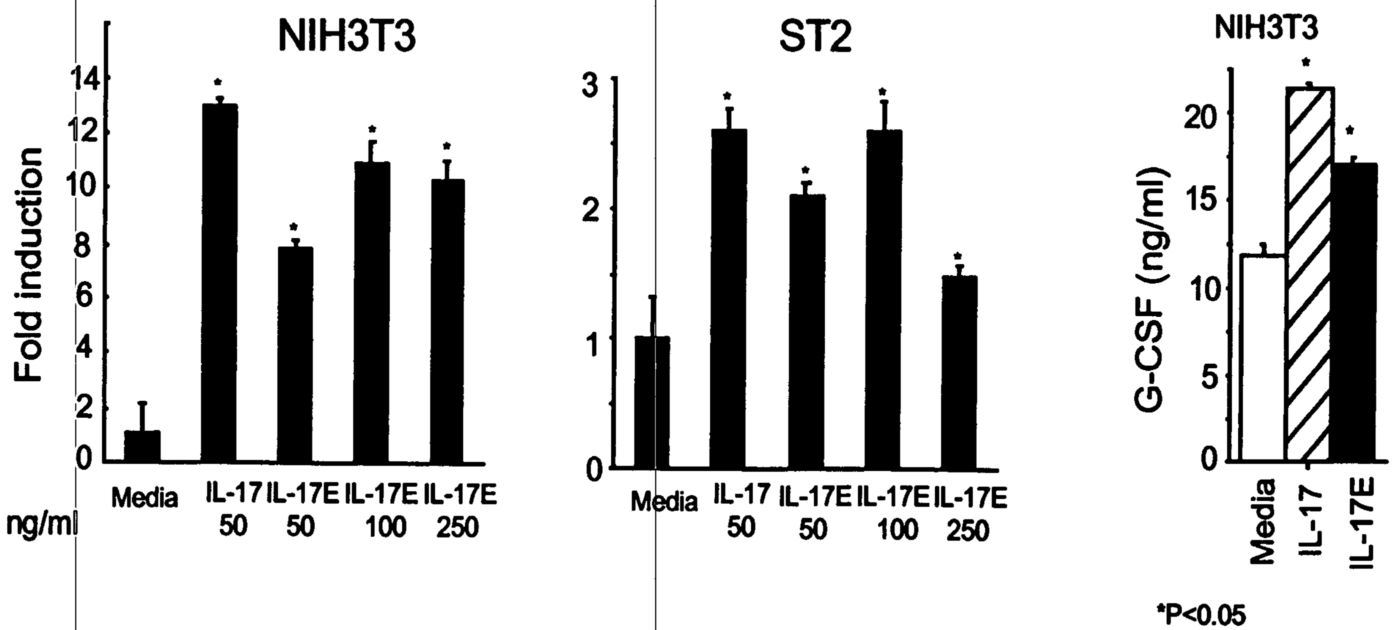


FIG. 65

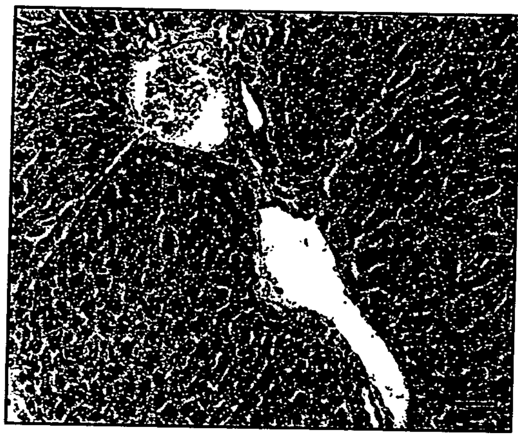


FIG. 66A

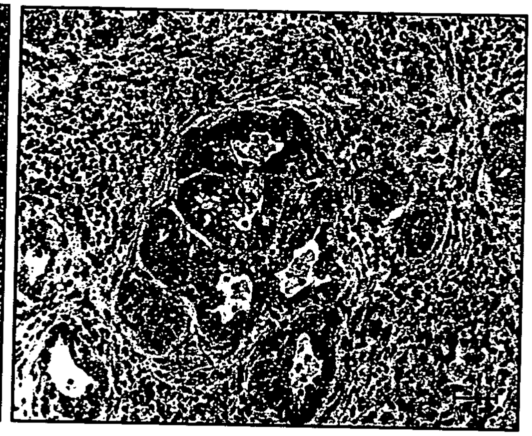


FIG. 66B

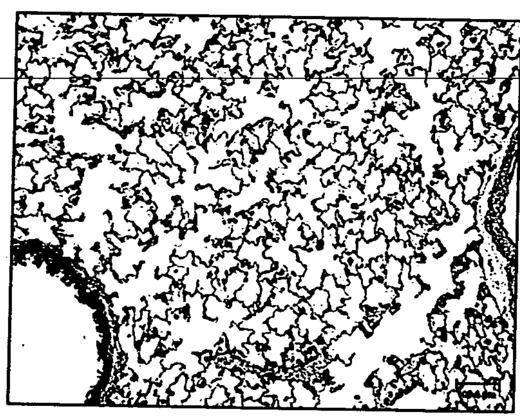


FIG. 66C

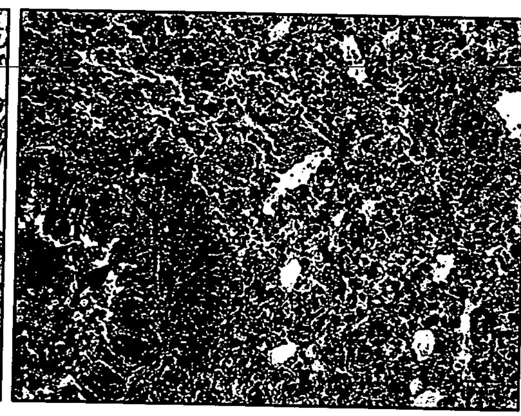


FIG.66D